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May 25, 2004, 04:22:47; Search time 4479.5 Seconds (without alignments) 16284.480 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	AX383954 Sequence	BD177602 Detection	S83182 hyaluronan-	AX409021 Sequence	D49742 Human mRNA	BC031412 Homo sapi	AX383955 Sequence	AK128915 Mus muscu	BC031775 Mus muscu	AL390197 Human DNA	AC006097 Homo sapi	AX305372 Sequence	ACLIS//1 Mus muscu	AC131859 Rattus no	AF099017 Mus muscu	AF224724 Mus muscu	BC019376 Mus muscu	I15469 Sequence 14	169315 Sequence 14	AX333070 Sequence	AX408965 Sequence	D14012 Homo sapien	X02/24 FOICING MEN	L03546 Bos taurus	E07615 DNA encodin	I15462 Sequence 3	I6930B Sequence 3	X63434 R DOTVEDICE	X02389 Mouse mRNA	A19618 Mammalian c	BC061565 Rattus no	M23697 Rat tissue-	A07248 / Desmodus to	A07250 Artificial	M63986 Desmodus ro	M63989 Desmodus ro	A07246 Artificial	108184 Sequence 4 J05082 Vampire bat			linear PAT 19-MAR-2002					Vertebrata; Buteleostomi; i; Hominidae; Homo.	:	ng,w., weimer,ï.,	rotease and methods for their
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182258-A 1 27-FEB-2002; ation/Qualifiers ation/Qualifiers ative anism="Homo sapiens" 1 type="unassigned DNA"	ATGITIGCCAGGAIGTCTGATCTCCATGITCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60	CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACATACC 180 [GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCTACTACTGCGTGTGTCTGTAAACAC 420	STCCCGAC STCCCGAC ATGGCTAC ATGGCTAC	TCTTACCGAGGGAAATGGAATAGGACAGCAGCGGCCTTACTGGAACTCC 660		TTGACTCC TTGACTCC
JOURNAL PA ATURES SOURCE GOURCE IGIN MATCH Best Local S	Qy 1 ATGTTTG Db 1 ATGTTTG Qy 61 GCCTGTG Db 61 GCCTGTG	Oy 121 CAGTATG Db 121 CAGTATG Oy 181 CATGCTG Db 181 CATGCTG	Qy 241 CCCTGTG Db 241 CCCTGTG Qy 301 GCTCCTT Db 301 GCTCCTT	Oy 361 GGCCGGG Db 361 GGCCGGG Oy 421 CCTTACA Db 421 CCTTACA	4 4 8 8 1 1 2 4 4 8 1 1 2 4 1 1 1 2 4 1 1 1 2 4 1 1 1 1	Oy 601 TCTTACC Db 601 TCTTACC OY 661 CACCTCC Db 661 CACCTCC	Cy 721 GGGGAAC Db 721 GGGGAAC Qy 781 GTTACCP	841

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OS HOME SADIES HERING GABH
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PD 2002291486-A/1
PD 08-OCT-2002
PF 25-JUL-2001 JP 2001224423
PR 26-JUL-2000 DE 10036641:4,10-OCT-2000 DE 10050040:4 PR 26-JUL-2000 DE 10036641:4,10-OCT-2000 DE 10052319:6,12-APR-2001 DE 1018706:8 PI LANG, PT 26-JUL-2000 DE 10052319:6,12-APR-2001 DE 1018706:8 PI LANG, PT THOMAS WEIMER, MARGRET BECKER, CLAUDIA NERLICH, GUDRUN MUTH PI NAUWANN
C C12N15/09,C07K16/40,C12N9/50,C12Q1/68,G01N33/53,G01N33/539, PC G1N33/535/C12P21/08,C12N15/00
CC Detection method with the use of factor VII activating CC protease mutant and CC specific antibody
FH Key Location Qualifiers
FT SOUTCE THE SOU Б ö CCCTGTGAA.CA.CGGTGGGA.CTGCCT.CGTCCATGGGAGCACCTTCA.CATGCAGCTGCCTG CCTTACACAGGTCCCCAGCTGCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC CAGITCAAGGGGAAATICIGIGAAATAGGITCIGATGACIGCIAIGITGGGGAIGGCIAC GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACTCGACCCTGAC CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCCATGCCAGCCCAAC GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT AIGTITGCCAGGAIGTCTGAFCTCCATGTTCTGCTGTTAATGGCTCTGGTGGAAAGACA CATGCTGAGAATCCTGACTACTACACTGAGGACCAAGCTGATCCATGCCAAGC ATGITTGCCAGGATGTCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA Gaps ; Length 1683; (human) Indels Vorce Location/Qualifiers

Nurce 1. 1683

Location/Qualifiers

1. 1683

Qorganism="Homo sapiens"

Acranism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606" .; 0 DB Query Match 100.0%; Score 1683; Best Local Similarity 100.0%; Pred. No. 0; Matches 1683; Conservative 0; Mismatches FFE Н source JOURNAL FEATURES TITLE COMMENT ORIGIN d ò g S 9 6 9 6 9 6 9 8 8 8

CAACTCTATGACCACATGATTGATGATCTGTGCAGGAAATCTTCAGAAACCT GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCTGACCTGTGAGAAGGACGCACC ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGGCCCAGGAC GCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGGTAGGGACCAGGACCTG TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC TACTACGETCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGGGGAAGAGGCCAGGGGTCTAC GITGCCTACCCAGAGAGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGGTTTGACTCC 1081 GCCCACTGCACCGACATAAAACCAGACATCTAAAGGTGGTGGTAGGGGACCAGGACCTG TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC CACCTCCTCTTGCAGGAGTTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT CACCTCCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT GGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA

1177 (106 961 1057 1117 1237 517 1021 1081 1141 1201 1297 277 337 397 361 457 421 481 577 541 601 661 721 781 181 241 301 d 8 & 8 8 8 8 8 8 8 8 8 8 8 8 g g 8 8 8 8 g ∂ ઠે 8 8 ò g ò d $\stackrel{>}{\circ}$ g $\dot{\delta}$ 8 PRI 11-FEB-1997 activator ö 120 156 216 180 276 and Tomita,M.

Purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and serine protease domain, similar to hepatocyte growth factor 9 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2408)
Choi Miura, N.H., Tobe, T., Sumiya, J., Nakano, Y., Sano, Y., Mazda, T. AIGITIGCCAGGAIGTCTCTGAICTCCAIGTTCTGCTGTAAIGGCTCTGGTGGGAAAGACA GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 179630] from the original journal article. This sequence comes from Fig. 3B.

Location/Qualifiers ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC Gaps ., DB 9; Length 2408; 983182 hyaluronan-binding protein=hepatocyte growth factor homolog [human, plasma, mRNA, 2408 nt]. 0; Indels J. Biochem. 119 (6), 1157-1165 (1996) 9642501 8827452 Query Match
100.0%; Score 1683;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1683; Conservative 0; Mismatches S83182.1 GI:1836158 sapiens (human) 1. .2408 TAA 1683 Ното 1681 97 61 157 121 1681 VERSION KEYWORDS SOURCE ORGANISM source DEFINITION REFERENCE AUTHORS JOURNAL MEDLINE PUBMED REMARK gene ACCESSION CDS FEATURES TITLE RESULT S83182 ORIGIN à d ð d 8 Q 8 a

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CATGCTGAGAATCCTGACTGCTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC
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1357 GATGGTCACTGTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCC 141.	21 TITCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGGTGTTACAGAAACAGAAAAGGG 1380	81 TCCGGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCGGC 1440	41 CAACTCTAIGACCACATGAITGAIGACAGTAIGATCTGIGCAGGAAATCTTCAGAAACCT 1500 	01 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGACGACGCTC 1560	1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGGGAAAGGCCAGGGGTCTAC	1621 ACCCAAGTTACCAAATTCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC 1680 	1681 TAA 1683 		HUMHGFAL 3008 bp mRNA linear PRI 10-FEB-1990 Human mRNA for HGF activator like protein, complete cds.	D49742. D49742.1 GI:736706 HGF activator like protein; serin protease. Homo sapiens (human)	Homo sapiens Bukaryotes, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia: Butheria: Primates: Catarrhini; Hominidae; Homo.	to 3008)	ompunished 2. (bases 1 to 3008) Kitamura,N.	Direct Submission Submitted (17-MAR-1995) Naomi Kitamura, Institute for Liver Research, Kansai Medical University, Moriguchi, Osaka 570, Japan
Db 13	Qy 1321 Db 1417	Oy 1381 Db 1477	Oy 1441 Db 1537	Qy 1501 Db 1597	Qy 150 Db 169	Oy 16: Db 17:	Qy 1681 Db 1777	RESULT 5	HUMHGFAL LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM	REFERENCE AUTHORS	ACTHORS AUTHORS	TITLE JOURNAL

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DEFINITION Human manA for HGF activator like protein, complete cds.

DEFINITION Human manA for HGF activator like protein, complete cds.

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HGF activator like protein, serin protease.

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Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2251)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McBwan,P.J.,
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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
B. 22388557 NSHLILLOENYNWEMEDAETHÖIGENPICRNPDADEKEWCFIKVTNDKVKWEYCDVSAC SADVAAPESESPTERSTLEPEDSCAKTEIRARIKKAIVGERSTAGAHPWAALOSS LPLIISMPQGHFCGGALIHPOWYLTAAHCTDIKTRHIKVVJGDQDLKKEEFFEGSFRV EKIFKYSHYNBRDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPDGSFPSGSECHIS GWGYTETGKGSRQLLDAKVKLIANTLCNSRQLYDFMIDDSMICAGNLQKPGQDTCQGD SGGPLTCEKGGTYXVYGIVSWGLECGKRPGVYTQVTKFLNMIKATIKSESGF" 657. 916 USA

NIN-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BOM-HGSC
Web site: http://www.ngsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A. Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: g Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20302151
Location/Qualifiers Ë Strausberg, R. Strausberg, R. Strausberg, R. Submission Submission Submitted (Gb-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

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Homo sapiens
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Mammalia; Butheria; Primatés; Catarrhini; Hominidae; Homo.
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Patent: EP 1182258-A 2 27-FEB-2002;
Aventis Behring GmbH (DE)
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241 CCCTGTGAACACGGTGGGGACTCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCTG 1 ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTGGCTCTGGTGGGAAAGACA AGGTTTGCCAGGATGCTTGTTGTTCTGCTGTGGGAAAGACA AGGTTTGCCAGGATGTCTGGTGGGAAAGACA AGGTTGTGCTTTAATGCCTGTGGGGAAAGACA CATGCTGAGAATCCTGACTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC CATGCTGAGAATCCTGACTACTACACTGAGGACCAGCTGATGCCATGCCAGCCCAAC GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAAAGTGCCATGT GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACGCGCTGTGTCTGTAAACAC CCTTACACAGGGCCCCAGCTGCTCCCAGGTTCCTGTATGCAGGCCAAACCCCTGCCAG AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC TCTTACCGAGGGAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC CACCTCCTCTTGCAGGAGATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCGGGGTTTGACTCC TGTGGAAAGACTGAGATAGCAQAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAACACCAGTAGCACTTACC CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC CAGTICAAGGGAAATICTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC GITGCCIACCCAGAGGAAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC Gaps Length 1683; ; 0 Indels 9 , , B Query Match
99.8%; Score 1679.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1681; Conservative 0; Mismatches 421 781 121 481 541 541 601 601 661 199 721 721 781 841 106 61 61 121 181 301 361 481 181 301 361 421 90 60 d g

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When the use of factor VII activating protease mutant and specific antibody.

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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Bookses 1 to 1683)

Roemisch, J. Stoehr, H.A., Feussner, A., Lang, W., Weimer, T., Becker, M., Nerlich, C. and Naumann, G.M.

Detection method with the use of factor VII activating protease mutant and specific antibody.

Detection method with the use of factor VII activating protease ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Louinted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0018, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO cDNA sequencing project supported by Ministry of Economy,

Trade and Industry of Japan; CDNA full insert sequencing: Research

Association for Biotechnology (RAB); ODNA ilbrary construction:

Helix Research Institute (HRI) (supported by Japan Key Technology

Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and

Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ainomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,R., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
Unpublished
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Mus musculus cDNA fis, clone TRACH2024735, moderately similar to HOMO ospiens hyaluronan binding protein 2 (HABP2).

AK128915

AK128915.1 GI:34536572

AK128915.1 GI:4611 insert sequence).

Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/mol_type="mRNA"
/mol_xref="taxon:10090"
/clone="TRACH2004735"
/note="cloning vector: pME18SFL3"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, R., Butcow, K.H., Schaefer, C.F., Batc, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Mans, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavanch, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Abramson, R.D., Mullahy, S.J., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallek, J.A., Gunarathe, F.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sockersen, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Mers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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1556 GGATCAGACACCTGCCCAGGTGACTCGGGGGCCCTCTAACCTGTGAGAAGGATGGAACT 1615
                                                                                                                                                                                                                                                                                                                                                                                                                     1676 ACTCAAGTCACCAAGTTCCTGAATTGGATAAAGACCACCATGCACAGGGAGGCTGGCCTC 1735
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 2119)
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                                                                                                               CAACTCTATGACCACACCACCACGATGACGAGATTGTGCGGGGAACCTTCAGAAGCCC
                                                                                                                                                                                                                                                                                                   1616 TACTACGTCTACGGGATTGTAAGCTGGGGCCAGGAATGTGGGAAGAAGCCAGGAGTCTAC
                                                                                                                                                                                                                                                                                                                                                                        1621 ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC
                                                                       CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT
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Tissue Procurement: Jefferg E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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Contact: MGC help desk
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 37 Row: n Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22122612. Location/Qualifiers
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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/clone="MGC:28705 IMAGE:4242577"
/tissue type="Kidney, normal. 5 month old male mouse."
/clone_lib="NCI CGAP_Kid14"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6"
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/note="Tryp SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:smart00020"
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/note="synonyms: MGC28705, HABP, PHBP, HGFAL"
/db_xref="LocusID:226243"
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/note="XR; Region: Kringle domain"
/db xref="CDD:smart00130"
866. .1579
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/mol_type="mRNA"
/strain="FVB/N"
                                                                          Sequencing Center
Center code: BCM-HGSC
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99 151 CCTCTCCAAAGACCACCTCCTCCTCAACCTCTATCCAACTCTCAACCTCCAACTCTCAACCTCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCA
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Sinth, D.R.

Sequencing of Human Chromosome 10

AL Unpublished

(E. 2 (bases 1 to 157750)

NRS Smith, D.R.

Smith, D.R.

Smith, D.R.

Smith, D.R.

Smith, D.R.

Smith, D.R.

Shows a to 157750

NAL Street, Waltham, MA 02154, USA

Street, Waltham, MA 02154, USA

Thors: Clone was sequenced in 1996 using Multiplex DNA Sequencing

T Pechnology. Data may contain low quality seq uence and BAC/Cosmid

vector sequences.

T NoTE: This is a "working draft' sequence. It currently

* NOTE: This is a "working draft' sequence. It currently

* Consists of 1 contigs Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* the accession number will be preserved.

* This sequence will be preserved.

* the accession number will be preserved.

* Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 10 clone CIT9878K-1031G15 map 10g25. AC006097. GI:3962469
HTG. HTGS. PHASE2; HTGS_CANCELLED. Homo sapiens (human)
Bukarvet
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                                                                                                                                                                                                                                                                                                                        96299 GCGTCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGT 96358
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157750)
                                                                                                                                                                   96179 ACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAG
                                                                                                                                                                                                                                          GOGICCCICCAGICCTCGCTCTGACCATCTCCATGCCCCAGGGCCACTCTGTGGT
                                                                                                                                                                                                                      925 AGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGCACGGCGGGCAAGCACCCATGGCAG
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                                                                                                             GAATAGCACAATTTATCTTTCTTGTGTCCCACAGACGTTGCCTACCCAGAGGAAAGCCCC
                                                                                                                                                   ACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAG
                                                Gaps
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                                                Indels
                                              18;
             DB 9;
           Query Match
15.5%; Score 261.2; DB 9
Best Local Similarity 93.8%; Pred. No. 1.2e-66;
Matches 272; Conservative 0; Mismatches 18
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Matches 270
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AC006097/C
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                                                                                         984
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1543 TGTCAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 İGTGAĞAAĞĞATĞĞAĞTTACTAÇĞTÇTACĞĞĞATTĞTAAĞCTĞĞĞĞÇCCAĞĞAATĞTĞĞĞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 AAGAAGCCAGGAGTCTACACTCAAGTCACCAAGTTCCTGAATTGGATAAAGACCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1363 ACAGAAACAGGAAAAGGGTCCCGGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 ACAGAAACAGGGGAAGGGTCCCGCCAGCTCCTGGATGCTAAAGTCAAACGTAATCGCTAAC
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                                                                                                                      GGGTCCCTCCAGGCCTGCCTGACCATCTCCATGCCCCAGGGCCACTCTCTGTGGT
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                                                                                                                                                                                  985 GCGTCCCTCCAGTCCTCGCCTCTCTGACCATCTCCATGCCCCCAGGGCCACTTCTGTGGT
865 ACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGGAAAGACTGAGATAGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa, K., Asal, S., Takahashi, Y., Nagata, T. and Ishii, Y. Method for examining ischemic conditions
Patent: WO 0188188-A 123 22-NOV-2001;
School Juridical Person Nihon University (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                 1045 gagacacratarcacccracragaracracracracraccacracraca 1094
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14.4%; Score 242.6; DB 6; Length 397;
Best Local Similarity 84.7%; Pred. No. 2.3e-61;
Matches 272; Conservative 0; Mismatches 49; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Mus musculus
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805 GAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGACGTTGCCTACCCAGAGGAAAGCCCC

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AC115771 204214 bp DNA linear HTG 18-JUN-2003
Mus musculus clone RP23-116D4, WORKING DRAFT SEQUENCE, 11 ordered
                                                                                                                                                             Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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ACI15771.4 GI:31880182
HTG; HTGS PHASE2; HTGS_FULLTOP.
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Mus musculus
                                                                                                                                                                                                                      Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-116D4 Unpublished
                                                                                                                                                                                                                                                                                 (bases 1 to 204214)
                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                      LOCUS
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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AC115771
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Contact: sequence submissions@genome.wi.mit.edu
Center project Information
Center project name: L15 D 4
Center clone name: L16 D 6
Center clone name: L16 D 7
Center clone name: L16 D 8
Center clone name: L16 D 8
Chemistry: Dy-terminator Big Dye; 100% of reads
Chemistry: Dy-terminator Big Dye; 100% of reads
Consensus quality; 202481 bases at least Q20
Consensus quality: 202492 bases at least Q20
Consensus quality: 202412 bases at least Q20
Consensus quality: 20242 bases at least Q20
Consensus qual

Birren, B. Lincon, L., Nuchaum, C., Lander, E., Ali, A., Allen, N., Anderno, E., Barra, N., Bastien, V., Bloom, T., Bouglaxdry, L., Colnogol, A., Gongo, J., Gangoo, J., Gollymore, A., Cooke, A., Cooke, P., DeArellano, K., Dawar, K., Dai, J., Ghoepel, Y., Colangoo, D., Galagain, J., Gardyna, S., Farro, E., Choepel, Y., Colangoo, D., Galagain, J., Gardyna, S., Gook, A., Cooke, P., DeArellano, K., Dawar, K., Langar, J., Gardyna, S., Gangoo, J., Horton, L., Athles, W., Tilley, I., Obnson, R., Jones, C., Kamat, A., Karlas, A., Kalls, C., Lakocque, K., Changare, R., Jones, C., Macdonaid, S., Gord, J., Levins, R., Lindhal-Toh, K., Marchan, C., Madonaid, J., Marguis, N., Marchan, C., Madonaid, P., Marchan, K., Maldina-Toh, R., Marchan, C., Madonaid, P., Marchan, K., Maldina-Toh, R., Marchan, C., Madonaid, J., Repart, J TITLE JOURNAL TITLE JOURNAL AUTHORS REFERENCE

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**NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**This sequence will be preserved.

**Tof63 71433: contig of 671 bp in length 71534: gap of 100 bp 72472 73321 contig of 100 bp 72472 73321 contig of 1449 bp in length 73371 72471: gap of 100 bp 72472 73920: contig of 1449 bp in length 73921 74020: gap of 100 bp 7445 bp in length 76566 86603: contig of 16553 bp in length 76566 86603: contig of 16553 bp in length 103257 117661: contig of 1653 bp in length 113603 135962: contig of 18305 bp in length 113603 135962: contig of 18305 bp in length 113603 135962: contig of 18305 bp in length 113603 131391: contig of 22723 bp in length 11392 131391: contig of 22723 bp in length 11392 131391: contig of 22723 bp in length 11392 131392: contig of 22723 bp in length 11392 139419: contig of 22723 bp in length 11394192 204214: contig of 22723 bp in length 11392 1394193 139419: contig of 22723 bp in length 11394192 1
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1. 70662
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ORIGIN

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RESULT 15 AC106236/c

Rattus norvegicus clone CH230-131J10, WORKING DRAFT SEQUENCE, 2 unordered pieces.
AC106236
AC106236
HTG5 HTG5 PHASE1; HTG5_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat.)
Bukarvora... LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Ruzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

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Cardenas, V., Carter, R., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, G.,

Davila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,

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Dayer, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Svans, C.A., Falls, T., Fan, G.,

Francacc, F., Falley, M., Flagg, N., Forbes, L., Foster, M.,

Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T.,

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Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, T.,

Jackson, L., Jacob, L., Jang, H., Johnson, R., Johnson, R., Johnson, R.,

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Lorenbuhewa, L., Loulseged, H., Levan, J., Lui, X., Mangum, A.,

Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K.,

Maheshwari, M., Manindartne, M., Mahmoud, M., Malloy, K., Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavijevic, A., Miner, G., Miloja, E., Wontemayor, J., Moore, S., Milosavijevic, A., Miner, G., Miloja, E., Wontemayor, J., Moore, S., Milosavijevic, A., Miner, G., Miloja, B., Montins, M., Mooris, K., Mooris, K., Mooris, K., Mooris, K., Mooris, K., Mooris, K., Mooris, C., Meal, D., Mooris, K., Mooris, G., Mooris, C., Meal, D., Mooris, K., Mooris, S., Mooris, C., Meal, D., Mooris, K., Mooris, G., Mooris, C., Meal, D., Mooris, A., Mooris, R., Mooris, C., Paterenak, S., Paul, H., Perce, A., Perce, M., Reiger, M., Reill, M., Scher, M., Scher, M., Reill, R., Mill, R., Mell, M., Reill, M., Reill, M., Reill, M., Reill, R., Marke, M., Reill, R., Marke, M., Margh, M., Marg

TITLE JOURNAL REFERENCE

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COMMENT

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center ode: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contear: hgsc.help@bom.tmc.edu
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Center project Information

data.html). NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

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10928 AGCACAGGGGCAAGCACCCGTGGCAGGTGTCCCTGCAGCACCTCATTGCCGCTGACCACC 70869
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Best Local Similarity 76.7%; Pred. No. 2.4e-36;
Matches 197; Conservative 0; Mismatches 60; Indels 0; Gaps
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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196131 224208: contig of 27978 bp in length.
196231 224208: contig of 27978 bp in length.
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Search completed: May 25, 2004, 09:00:30 Job time : 4486.5 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

May 25, 2004, 04:19:43 ; Search time 471 Seconds (without alignments) 15179.867 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-912-559-1 1683 1 atgtttgccaggatgtctga.....aaagtgaaagtggcttctaa 1683 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched: 6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:*geneseqn2003cs:* N_Geneseq_29Jan04:* 1:_ geneseqn1980s:* geneseqn2004s:* geneseqn1980s:* geneseqn1990s:* .01 .01 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	6 Human	170 Gene #	04 Human	Aal45697 Human blo	Aac76693 Human ORF	3 Human	Human	1 Mouse	Human	Probe	Human	Human	Abs31791 Human liv	Abs06863 Human gen	Aaq63951 Hepatocyt	Lung	Gene #	Human	Aai51106 Probe #19	Aak45153 Human bon	Aak19188 Human bra	Abs44824 Human liv	Abs19403 Human gen
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Claim 2; Page 15-16; 27pp; German

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ALIGNMENTS

New nucleic acid encoding mutant factor 7 activating protease, useful for diagnosis, treatment and prevention of coagulation disorders, also related protein and antibodies. Human; blood coagulation factor VII activating protease; FSAP; single-chain plasminogen activator; bleeding disorder; haematological; haemostatic; gene; ds. Becker M; Human blood coagulation factor VII activating protease DNA. Weimer T, Lang W, Location/Qualifiers 1. .1683 /*tag= a /product= "FSAP" Roemisch J, Stoehr H, Feussner A, Nerlich C, Muth-Naumarn G; BP. 26-JUL-2000; 2000DE-01036641. 10-OCT-2000; 2000DE-01050640. 10-OCT-2000; 2000DE-01052319. 12-APR-2001; 2001DE-01018706. 05-JUL-2001; 2001EP-00115691. (AVET) AVENTIS BEHRING GMBH AAL45696 standard; DNA; 1683 13-JUN-2002 (first entry) WPI; 2002-270939/32. P-PSDB; AAO17144. EP1182258-A1 Homo sapiens 27-FEB-2002. AAL45696; RESULT 1 Key us-09-912-559-1.rng

Page 2

901 TGTGGTAACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTT 901 TGTGGAAAGATGAGAAGAGGAAGAAGAACATCAACCAAGCTTCCGGGGTT 901 TGTGGAAAGATGAGAAAGAGAAGAAGAACATCAAAGAAATCTATGGAGGCTT 961 ACGGCGGGCAAACACACATGCAGAGAGAACATCAAGAAATCTATGGAGGCTT 961 ACGGCGGGCAAACACATGCAGGAGGACCTCCAATCTATGGAGGCTT 961 ACGGCGGGCAAACACATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGAC 1021 ATGCCCAGGGCCACTTCTGTGGTGGGGGGCCTGATCCACCCTGTGCTGCTCTGAC 1021 ATGCCCAGGGCCACTTCTGTGGTGGGGGGGCTTCCTCTGACCCTGTGGGTGCTTCTAACACACAC	Oy 1081 GCCCACTGCACCACATAAAACCAGACATCTAAAGTGTGGGGACCTGCAGACACTCTAAGGTGGTGGGGACCAGACCTG 1140 Db 1081 GCCCACTGCACTAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG 1140 Oy 1141 AAGAAAGAAGAATTTCATGAGCAGACTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC 1200 Db 1141 AAGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC 1200 Oy 1201 TACAATGAAAGAATTCCCCCACAATGATATTGCATTGCTTCAGTTAAAGCCAGTG 1260	1201 TACAATGAAAGAGATGCCCCCCCCCCAATGATTGCATTGCTCCAAGTTAAAGCCAGTG 1261 GATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGTGTGCTTGCT	Db 1321 TTTCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGTGTTACAGAAACAGGAAAAGGG 1380 Qy 1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACATTGTGCAACTCCGGC 1440 Db 1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTCAATTGCCAACATTTGTGCAACTCCGGC 1440 Qy 1441 CAACTCTATGACCACATGATGATGATGAATGTGTGTGCAGAAATCTTGTAGAAACCT 1500	1441 1501 1501	OY 1561 IACING CITAL CONTROL C	1681 TAA	RESULT 2 ABN95170 ID ABN95170 standard; DNA; 3008 BP. XX AC ABN95170; XX XX DT 13-AUG-2002 (first entry)	ne #1668 used to d ne; liver cancer; tastatic liver tum sease progression;
CC The present invention relates to a mutant of the DNA sequence encoding the processes (FSAP) that activates blood coagulation factor VII (FVII) CC and single-chain plasminogen activator, where at least one of the base CC changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is CC blood coagulation sequences can be used in the treatment and prevention CC blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's CC blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's CC sequence is the human FSAP coding squence CC sequence 1683 BP; 440 A; 436 C; 437 G; 370 T; 0 U; 0 Other; Query Match Query Match Rest Local Similarity 100.0%; Score 1683; DB 6; Length 1683; Best Local Similarity 100.0%; Pred, No. 0; Namanches 1683; Onservative 0; Masmatches 0; Indels 0; Gaps 0;	1 1 2 1 1 1	121 CAGTATGAGATACAGAGATTATAATCAGGAAGAACACCAGTAGCACTTACC 181 CATGCTGAGAATCCTGACTGAGTGACTCAGGAAGAACACCAGTAGCACTTACC 181 CATGCTGAGAATCCTGACTGATTATAATCAGGACCAAGCTGATCCATGCCAGCCCAAC	241 CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACTTCACATGCAGGTGCCTG 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACGACGAACCATGT 10	Qy 361 GGCGGGGGCCAATGTCTCATTACCCAGGTCCTCCTACTACTGTCTGT	QY 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGGC 540 Db 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACTGTGCCTGTCCGGAC 540 QY 541 CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTATGTTGGCGATGGCTAC 600 Db 541 CAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTACTTGTGGCGATGGCTAC 600	OY 601 TCTTACCGAGGGAAATGAATGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 660 	Oy 661 CACCTCCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 720	781 GTTACCAATACAAGGGAAATACGGAATACTGTGATGCTCAGGCTGCTCAGGACCAGGAC

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                                                                                                                                                                                                                                                                                    Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
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ö 156 120 GCCTGTGGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 216 180 CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCGAGCCCAAC 240 CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 336 GGCCGGGGCCAATGTCTATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC 420 276 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 360 CCCTGTGAACACGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 300 9 ATGTTTGCCAGGATGTCTGATCTCCATGTTAATGGCTCTGGTGGGAAGACA CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAACACCCAGTAGCACACTTACC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAACAACCAGTAGCACATTACC ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA GCCTGTGGGTTCTCCCTGATGTTTTGGAAAGCCTGGACCCAGACTGGACCCCTGAC Gaps ö DB 6; Length 3008; Indels 0; Query Match 100.0%; Score 1683; Best Local Similarity 100.0%; Pred. No. 0; Matches 1683; Conservative 0; Mismatches 97 61 157 121 217 181 277 337 301 397 361 241 457

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1116 1140 1320 1380 1056 1020 1080 1176 1236 1200 1296 1260 1356 1416 1476 1536 1560 540 636 600 9 756 720 816 780 876 840 936 900 966 960 480 576 969 TGTGGAAAGACTGAGATAGCAGAGAGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC GATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCC TTTCCTCTGGGAGTGAGTGACTATCTCTGGCTGGGGTGTTACAGAAACAGGAAAAGGG TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGGCCCAGGAC 1081 GCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG
1177 GCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGGTAGGGGACCAGGACCTG TACAATGAAAGAAGATGAGATTCCCCACAATGATATTGCATTGCATTGCATTAAAGTTAAAGCCAGTG CCTTACACACGCTCCCAGCTGCTCCCAGTTCCTGTATGCAGGCCAAACCCCTGCAG AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCAAC CAGTICAAGGGAAATICTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGGCCAGGAC GTTGCCTACCCAGAGAAAGCCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC GTTGCCTACCCAGAGGAAGCCCCCACTGAGCCATCAACCAAGCTTCGGGGTTTGACTCC AAGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC TACAATGAAAGAGATGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG CAACTCTATGACCCACATGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT CAACTCTATGACCACACTGATGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC GTCCCGAC TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 1357 (1021 1117 1141 1237 1201 1297 1261 1321 1417 1381 1477 1441 1501

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1680 1776

U; 0 Other

Sequence 3008 BP; 791 A; 837 C; 703 G; 677 T; 0

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1656

RESULT

ACC51204 standard; cDNA; 3008

BP.

(first 16-JUN-2003

Human Plk-1 related cDNA seguence hmft-0306 SEQ ID NO:89.

Human; hepatoblastoma; cancer detection probe; cancer; detection; hepatocallular carcilioma; hereditary non-polyposis colorectal cancer; desmoid tumour; anaplastic thyroid carcinoma; Wilm's tumour; tumour; Plk-1; polo-like kinase-1; gene; ss.

Homo sapiens

WO2003018807-A1.

06-MAR-2003

26-AUG-2002; 2002WO-JP008580.

24-AUG-2001; 2001JP-00255225.

CO LID (HISM) HISAMITSU PHARM ((CHIB-) CHIBA PREFECTURE.

Nakagawara A;

WPI; 2003-268424/26.

Nucleic acid sequences differently expressed between hepatoblastoma and normal liver tissue, are useful for cancer detection and diagnosis.

Claim 4; Page 142-144; 180pp; Japanese.

The present invention describes mucleic acid sequences (I) having a different degree of expression in hepatoblastoma from their expression in concurrent issue. ACC51116 to ACC51219 represents specifically claimed examples of (I). Also described: (I) nucleic acids stringently camed examples of (I). Also described: (I) nucleic acids stringently or more of hybridising to (I); (2) cancer detection probes containing one or more of configuration of the concertain sequences derived from them; (3) sea ACC51116 to ACC51219, including the 79 (I, sea ACC51116 to ACC51194), or partial sequences (II); (4) marker or proteins for cancer detection, encoded by (II); (5) diagnostic reagents or cancer diagnosis, containing (II) or their partial sequences. The nucleic acid sequences are useful in the detection and diagnosis of cancers including liver, colon, breast, kidney, bladder, overy and thyroid cancer, especially for hepatoblastoma, hepatocellular carcinoma, hereditary non-polyposis colorected cancer, desmoid tumour, anaplastic thyroid carcinoma and Wilm's tumour. They are also used as markers for predicting the prognosis of these tumours, ACC51220 to ACC51231 represent PCR primers used in the exemplification of the present invention. The nucleic acid sequences given in ACC51116 to ACC51219 are related to human or ply-1 (polo-like kinase-1), which is located on chromosome 16p12

1116 1056 120 216 180 276 240 336 300 396 360 516 480 576 540 600 969 99 756 720 816 780 876 840 936 966 960 156 456 420 989 CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC GGGGAACACAATTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA GCCTGTGGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAAGAACACCAGTAGCACTTACC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAAGAACACCCAGTAGCACTTACC CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGGAC ATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGAATT GGGGAACACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC GITGCCTACCCAGGGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC 997 IGIGGAAAGACTGAGATAGCAGAGAAGAACATCAAGAGAATCTATGGAGGCTTTAAGAGC ACGGCGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGACCATCTCC GCCTGTGGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC GGCCGGGGCCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTGTAAACAC CAGTICAAGGGGAAATICIGTGAAATAGGTICIGATGACTGCTATGTIGGCGATGGCTAC TGTGGAAAGACTGAGATAGCAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC TCTTACCGAGGGAAATGGATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 0; Length 3008; 1 ATGITTGCCAGGATGTCTGATCTCCATGTTCTGCTGATGGCTCTGG Indels DB 7; .; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1683; Conservative 0; Mismatches 97 61 157 121 217 181 277 241 337 301 397 361 457 517 481 577 541 637 601 697 661 757 721 817 781 877 841 937 901 961 421 Query Match g q g ď QQ 8 8 d q g g ò g ò à à ò ŏ ò d ò qq δ g ò g ò Q ò ઠે ò ò

May 2/ 10:53:53

1440 1560 1716 1536 1500 1596 1656 TITCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGGTGTTACAGAAACAGGAAAAGGG 1380 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACTGTGAGAAGGACGGCACC GGGCAAGACACCTGCCAGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGAAGGCCAC GATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCC TTCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGTGTTACAGAAAAGAGGAAAAGGG TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC CAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1537 CAACTCTATGACCACATGATGATGACAGTATGATGATCTGTGCAGGAAATCTTCAGAAACCT ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC AIGCCCCAGGGCCACTTCTGTGGTGGGGGGGCGCTGATCCACCCCTGCTGGTGGCTCACTGCT GCCCACTGCACCGACATAAAAACCAGACATCTAAAAGGTGGTGCTAGGGGACCAGGACCTG AAGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC GCCCACTGCACCGACATAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG TACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG TAA 1683 TAA 1779 1657 1621 1477 1597 1561 1141 1237 1297 1357 1321 1417 1381 1441 1501 1117 1081 1177 1201 1261 ВЪ Q ò ДĎ δ ò 임 8 8 S Q \$ B 8 B 8 БÞ ò g 8 S δ

AAL45697 standard; DNA; 1683 (first entry) 13-JUN-2002

Human blood coagulation factor VII activating protease mutant DNA

Human; blood coagulation factor VII activating protease; FSAP; single-chain plasminogen activator; bleeding disorder; haematological; haemostatic; mutant; gene; ds.

Homo sapiens Synthetic.

Location/Qualifiers 1. .1683 /*tag= a /product= "mutant FS?

EP1182258-A1

2001EP-00115691 05-JUL-2001; 27-FEB-2002

26-JUL-2000; 2000DE-01036641. 10-OCT-2000; 2000DE-01050040. 21-OCT-2000; 2000DE-01052319. 12-APR-2001; 2001DE-01018706.

AVET) AVENTIS BEHRING GMBH

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Ξ Becker WPI; 2002-270939/32. P-PSDB; AAO17145.

The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the mutant human FSAP coding squence SX CCCCCCCCXXXX T T X X B X X B X X B X X B X X B X X B X X B

Sequence 1683 BP; 441 A; 437 C; 435 G; 370 T; 0 U; 0 Other;

Query Match
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1681; Conservative 0; Mismatches 2; Indels 0;

9 1 ATGITIGCCAGGAIGTCTGAICTCCAIGTICTGCTGAATGGCTCTGGTGGGAAAGACA

120 180 180 GCCTGTGGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACATTACC 61 121 g d à ò

240 240 CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATGCCATGCCAAG 181 181 $\dot{\delta}$ 엄

420 480 480 certracacacacacacacacacacas and a serio construction and a serio construction of the serio constr 361 421

540 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC 481

Weimer T, Lang W, Stoehr H, Feussner Muth-Naumann G; Roemisch J, Nerlich C,

for New nucleic acid encoding mutant factor 7 activating protease, useful diagnosis, treatment and prevention of coagulation disorders, also related protein and antibodies.

Disclosure; Page 16-17; 27pp; German.

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CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC

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420 GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCTACTACCCGCTGTGTGTAAACAC 361

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1021 ATGCCCCAGGGCCACTTCTGTGTGGGGGGGCGCTGATCCACCCCTGCTGGGGCCACTGCTGCTCACTGCT 1021 ATGCCCCAGGGCCACTTCTGTGGTGGGCGCTGATCCACCCCTGCTGGTGCTCACTGCT GCCCACTGCACCACATAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG 1081

1201 1201 1261

TITCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGGTGTTACAGAAACAGGAAAAGGG 1380 1321 TTTCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGGGTGTTACAGAAACAGGAAAAGGG TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 1381 1321

TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCGAACTCCCGC

CAACTCTATGACCACATGATTGATGACAGTATGATCGATGCAGGAAATCTTCAGAAACCT CAACTCTATGACCACATGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC 1501 1441 1441

1621 ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGGCCACCATCAAAAGTGAAAGTGOCTTC 1681 TAN 1683 TAA 1683 1681 g g ò

> 999 9 720

1561 TACTACGTCTATGGGGTAGTGAGCTGGGGCCTGGAGTGTGAGAAGAGGCCAGGGGTCTAC ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC

1621

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BP AAC76693 standard; cDNA; 3623

AAC76693;

780

08-FEB-2001 (first entry)

900 900 960 096

840 840

Human ORFX ORF2248 polynucleotide sequence SEQ ID NO:4495.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; immunostimulant; osteopathic; antiarthritic; immunosuppressant; cardiant; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antitihamatory; antitianemic; gene therapy; antifungal; antirhematic; antithyrolid; antichyrolid; sascular disease; diabetes mellitus; hypothyroldism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss. RESULT 5
TO 6693
TO 6693
TO 6693
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TO 6693
TO 6993
TO 69

Homo sapiens.

WO200058473-A2.

1140 1140

1080

05-OCT-2000.

31-MAR-2000; 2000WO-US008621

31-WAR-1999; 99US-0127607P. 02-APR-1999; 99US-0127636P. 05-APR-1999; 99US-0127728P. 30-WAR-2000; 2000US-00540763.

(CURA-) CURAGEN CORP.

1260

1200 1260 Leach M;

Shimkets RA,

WPI; 2000-602362/57. P-PSDB; AAB42484.

Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

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Claim 5; Page 3679-3681; 5507pp; English.

1440

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1560

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which represent the human ORFX open reading frames 1 to 3161. The ORFX which represent the human ORFX open reading frames 1 to 3161. The ORFX acquences have activities such as: oytostatic; hepatotropic; vulnerary; antipacriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; deradiant; thrombolytkic; coagulant; vasotropic; antidiabetic; hypotensive; dermacological; immunosuppressive; antinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antinflammatory; antibacterial; acquences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX

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TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGGGGAAGAGCCAGGGGTCTAC

1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC

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QQ	937 GITGCCTACCCAGAGGAAAGCCCCACTGAGCATCAACCAAGCTTCCGGGGTITGACTCC 996
ò	01 TGTGGAAAGACTGAGATAGCAGAGAGAAGATCAAGAAGAATCTATGGAGGCTTTAAGAGG 960
qq	97 IGTGGAAAGACTGAGATAGCAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAAAGC 105
òá	961 ACGGCGGCAAGCACCCATGGCAGCGTCCCTCCAGTCCTCGGTGCCTCTGACCATCTCC 1020 1051
3 8	021 AIGCCCCAGAGCCACTICIGNGGAGGCGCTGATCCACCCCTGCTGGGGGGTGCTCACTGCT 108
2 d	117 ATGCCCCAGGCCACTTCTGTGGTGGGCACTGATCCACCCTGCTGGGTGCTCACTGCT
ò	1081 GCCCACTGCACCACATAAAACCAGACATCTAAAGGTGGTGGTGGGGGACCAGGACCTG 1140
qq	CACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGG
š	41 AAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC 120
셤	37 AAGAAAGAAGAATTTCATGAGCAGGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC 1290
ð i	201 TACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG 126
g (297 TACAATGAAAGAGATTCCCCACAATGATATGCATTGCTCAAGTTAAAGCCAGTG
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3 8	
S 8	11
È	381 TCCCSCCAACTCCTCAATGCCAAAGTCAAGGTGATTGCCAACATTGGGAACTCCCGC 144
. 심	477 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 153
ò	1441 CAACTCTATGACCACATGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500
q	1537 CAACTCTATGACCACATGATTGATGACAGTATGATCGATGCAGGAAATCTTCAGAAACCT 1596
ò	1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC 1560
q	CAGGGTGACTCTGGAGGCCCCCTGACTGTGAGAGGACGC
ò	162
Op	-[]
ò	1621 ACCCAAGTTACCAAATTCCTGAATTGGATCAAGGCCACCATCAAAAGTGAAAGTGGCTTC 1680
qq	-63
ò	1681 TAA 1683
qq	1777 TAA 1779
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us-09-912-559-1.rng

Thu May

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AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (BESTS), isolated from human, mouse, chicken and rat tissue conscrees. The SESTS can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; analgesic; nationally antifungal; antivital; antidiabetic; antiasthmatic; vulnerary; antibacterial; antifungal; antivital; antidiabetic; antiasthmatic; vulnerary; antibacterial; costeopathic; neuroprotective; notropic; antidepressant. The SESTS can be used for gene therapy and in vaccines. The SESTS are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA conceptor and isolation of full-length cDNAs and genomic DNA contibuted in assays for determining biological activity and raising antible sclerosis, insulin dependent diabetes), altergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoprosis, osteoarthritis, central nervous system disorders (Alzheimer's Parkinson's, Huntington's disease, stroke), coagulation disorders (disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's coarlasts, AAA45926 to AAA45931 represent invention continue.)
thrombolytic, antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidabelic; antiasthmatic; vulnerary; antiparkinsonian; antiuler: osteopathic; neuroprotective; nootropic; antipasriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; parkinson; disease; Huntington's disease; stroke; parkinson; disease; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lavallie ER,
Bowman MR;
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Treacy M,
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                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                              20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs K, 1
Merberg D,
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Evans C;

Sequence 617 BP; 165 A; 169 C; 148 G; 135 T; 0 U; 0 Other;

0; Gaps Length 617; 1; Indels Score 526.4; DB 3; Pred. No. 3.1e-140; 0; Mismatches 1; 31.3%; 31.3* Query Match Best Local Similarity 99.8' Matches 527, Conservative

84 AIGTITGCCAGGAIGICTGAICTCCAIGTICTCGCIGITAAIGGCTCTGGGGAAGACACA 143 61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120 ATGITTGCCAGGATGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA

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eccrerecentric contration and a second CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAACACCAGTAGCACACTTACC 180

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480 420 503 563 300 360 443 323 383 corracacagereceaecrecreceaagregrecererargeaageceaaaceecrage CACGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC CCCTGTGAACACGGTGGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAAACAC correndado de encede de consecución d GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAAGGACAACCCATGT CATGCTGAGAATCCTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGT 528 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACTGT 611 324 384 444 564 241 361 421 481 204 181 264 301 δ ద ò 8 ò qq ò g ઠ g 8

ACH21030 standard; cDNA; 428 BP. Human adult liver cDNA #642 13-OCT-2003 (first entry) ACH21030;

ss; sequencing by hybridisation; SBH; expressed sequence tag; mapping; biodiversity; genetic disorder. Human; genome

US2003073623-A1. Homo sapiens

17-APR-2003.

30-JUL-2001; 2001US-00918995. 30-JUL-2001; 2001US-00918995

m (DRMA/) DRWANAC R T. (LABA/) LABAT I. (STAC/) STACHE-CRAIN E (DICK/) DICKSON M C. (JONE/) JONES L W. LABAT I. STACHE-CRAIN

Jones LW; Dickson MC, Stache-Crain B, Drmanac RT, Labat I,

WPI; 2003-615964/58.

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cDNA libraries, useful chromosome and gene or in generating New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein, antisense DNA or RNA.

Claim 1; SEQ ID NO 8242; 44pp; English

The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polymetride comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences

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Takahashi Y,

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are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensits, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was sequence. Useful and in electronic format directly from USPTO at sequence. Language obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ischaemic condition related cDNA sequence SEQ ID NO:123
                                                                                                                                                                                                                                          Query Match
21.9%; Score 368.4; DB 8; Length 428;
Best Local Similarity 99.7%; Pred. No. 5.2e-95;
Matches 369; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                               Sequence 428 BP; 119 A; 108 C; 105 G; 96 T; 0 U; 0 Other;
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression profile of particular genes (ABI95020 to ABI99912, encoding the expression profile of a gene group comprising these genes. The expression profile of a gene group comprising these genes are used as an levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1363 ACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1423 ACTITGIGCAACTCCCGCCAACTCTATGACCACATGATGACAGTATGATCTGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity 84.7%; Pred. No. 6e-59;
Matches 272; Conservative 0; Mismatches 49;
Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human foetal liver single exon nucleic
                                                                                                                                    Claim 2; Page 351-352; 2690pp; English
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ABA58323 standard; DNA; 451
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   Asai S,
                              WPI; 2002-034733/04
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    Ishikawa K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 1.1%; Score 120.2; DB 4; Length 451; Local Similarity 97.6%; Pred. No. 8.1e-24; nes 122; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 6628; 639pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0660840B.
03-AUG-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000US-0234587P.
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Human genome-derived single exon nucleic acid probes useful for analyzing

DR; Rank 1

Chen W,

Hanzel DK,

SG, Penn WPI; 2001-488897/53

(MOLE-) MOLECULAR DYNAMICS INC

26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-023459P. 04-OCT-2000; 2000GS-00024263.

Claim 25; SEQ ID NO 6633; 654pp; English

gene expression in human placenta

The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for prodicting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders

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                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                  Length 451;
                                                                                                                                                                                                               Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                  7.1%; Score 120.2; DB 4; Length 97.6%; Pred. No. 8.1e-24; vative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed single exon probe SEQ ID NO:
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                             Best Local Similarity 97.6
Matches 122; Conservative
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                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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                                                            acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                  CAGAGACTCCTCCCTACTACGCTGTGTCTTAAAACACCCTTACACAGGTCCCAGCTGCTC
                                                                                                                                                                                                                                                                                                TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
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0
                                                                                                                                                                                                                                              DB 4; Length 451;
                                                                                                  4; SEQ ID NO 6653; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                    Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human brain expressed single exon probe SEQ ID NO: 6411.
                                                                                                                                                                                                                                          Query Match 7.1%; Score 120.2; DB 4; Best Local Similarity 97.6%; Pred. No. 8.1e-24; Matches 122; Conservative 0; Mismatches 3;
                                                            Human genome-derived single exon nucleic gene expression in human bone marrow.
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2000US-0204456P.

2000US-0069456P.

2000US-00632366.

2000US-0234687P.

2000US-0234687P.

2000GB-00024263P.
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            Hanzel DK,
                                     WPI; 2001-488900/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probes useful for analyzing
                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
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                                                                                                                                                              C; 127 G; 106 T; 0 U; 0 Other;
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97.6%; Pred. No. 8.1e-24;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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26-MAY-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00601408.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-0032459P.
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                                                                                                                                                              Sequence 451 BP; 116 A; 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coronary heart disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                       Query Match
Best Local Similarity 97.6
Matches 122; Conservative
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ABS31791/c
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Example 4; SEQ ID NO 6411; 650pp + Sequence Listing; English.

brains

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measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                       Length 451;
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97.6%; Pred. No. 8.1
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Matches 122;
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443
324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 383
                         CCAGAGTCCTCCCTACTACTGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC 332
                                                    CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC
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琚. ABS06863 standard; DNA; 451 (first entry) 19-AUG-2002 ABS06863; ABS06863,

Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interatitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; daucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary historycosis; lymphangloleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary dyskinesis; pulmonary hypertension; Human genome-derived single exon probe from lung SEQ ID No 6854. primary ciliary dyskinesi hyaline membrane disease.

Homo sapiens

WO200186003-A2.

15-NOV-2001

30-JAN-2001; 2001WO-US000665

; 2000US-0207456P. ; 2000US-00608408. ; 2000US-00632366. ; 2000US-0234687P. ; 2000US-0234687P. 2000GB-00024263 26-MAY-2000; 03-AUG-2000; 21-SEP-2000; 04-OCT-2000; (MOLE-) MOLECULAR DYNAMICS INC

DR; Rank Chen W, Hanzel DK, Penn SG,

ů set of single exon nucleic acid probes, used measure gene expression in human lung samples.

Claim 1; SEQ ID NO 6854; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thum lung comprising single exon nucleic acid probes having one of Iron human lung comprising the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid expressed in the human lung; measuring spee expression in a sample collection of detectably labeled nucleic acids derived from human lung; measuring spee expression in a sample collection of detectably labeled nucleic acids derived from human lung and the label detectably bound to each probe of the carry; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of algorithmically predicting at least one exon from genomic sequences of the enkaryote; and (b) detecting specific hybridisation of detectably, the above mentioned microarray; assigning exons to a single exon probe, in the above mentioned microarray; assigning exons to a single exon probe of the exons such the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon microarray bring a probe with the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon compression of the exons in the tissues and/or cell types indicates that expression of the exons in the tissues and/or cell types indicates that carryession of the exons should be assigned to a single gene; a peptide comprising one callysis, and for identifying exons in a gene, particularly using human lung derived manyas, and for the erudy of lung diseases such as asthma, under constructive pulmonary disease such as asthma, lung cancer, chronic obstructive pulmonary diseases such as asthma, lung derived manyas, gauchers of sisease (IDD), familial iddopathic pulmonary abrolar pa Karagener syndrome, fibrocystur, pulmonary dysplasis, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 U; 0 Other;

Gaps ., Score 120.2; DB 6; Length 451; Indels Query Match 7.1%; Score 120.4; C. Best Local Similarity 97.6%; Pred. No. 8.1e-24; Best Local Similarity 97.6%; Mismatches 3;

392 443 324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 451 recracadrecaaaaracerecaaedacaaeceareregeecegeeceaarerearrae 384 CCAGAGTCCTCCCTACTACCGCTGTGTGAAACACCCTTACACAGGTCCCAGCTGCTC g à 391 ccadadricticcractaccecraterereraaacacecraacacadarececaderecec

CCAAG 448 CCAAG 327 444 331 셤 ò

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AAQ63951 standard; cDNA; 2033 BP RESULT 15 AAQ63951

AAQ63951; SYSYST

(revised)
(first entry) 25-MAR-2003 06-JAN-1995

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"Hepatocyte growth factor converting protease."
                                                                                                                                                                                                                                                                              Hepatocyte growth factor converting protease and precursor and gene encoding them - for producing active two chain HGF from inactive single chain HGF.
                      Hepatocyte growth factor, protease, cleavage, active, inactive,
precursor, ds.
    Hepatocyte growth factor converting protease coding sequence.
                                                                                                                                                                                                                                  Kitamura N,
                                                                                                                                                                                                                                   Morimoto Y,
                                                                     Location/Qualifiers
1. .1968
/*tag= a
/product= "Hepatocytu
                                                                                                                                                                                                                                                                                                                      Claim 15; Page 26-27; 30pp; English.
                                                                                                                                                                           '92JP-00296133.
92JP-00312234.
92JP-00312242.
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                                                                                                                                                          93EP-00117988
                                                                                                                                                                                                                                    Shimomura T, Yamada K,
                                                                                                                                                                                                                                                      WPI; 1994-152921/19.
P-PSDB; AAR53962.
                                                                                                                                                                            05-NOV-1992;
20-NOV-1992;
20-NOV-1992;
                                                      Homo sapiens
                                                                                                                                                            05-NOV-1993;
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                                                                                                                                        11-MAY-1994
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Miyazawa

The polypeptide encoded by this sequence has protease activity and is capable of converting inactive single chain hepatocyte growth factor (HGF) into active two chain HGF by cleavage at a specific site. (Updated on 25-MAR-2003 to correct PN field.) Length 2033; Sequence 2033 BP; 339 A; 739 C; 623 G; 332 T; 0 U; 0 Other;

1098 1041 10; 765 825 TGCTCAGCCCAGGACGTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAAGCTT 885 585 645 705 981 861 921 801 GCCTGTCCCGACCAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGA---CTGCTAT CITIACIGGAACICCCACCICCICITGCAGAGAATIACAACAIGITTAIGGAGGAIGCT crescerdabacrecearerecreraciadas de crecacereca con esta en consecuencia en con GAAACCCATGGGGATTGGGGAACACTATTCTGCAGAAACCCAGATGCGGACGAAAAGCCC decergérgadecriadececedargecriacidecegaaréegaardadaagadee 586 GITGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTAGTCAACCAGCATGCGTGC TGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCC AACCCCTGCCAGAATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGT Accerridecendalededecaceredecendares de concesos de consecuencia de la 54; Indels Query Match 7.0%; Score 117.6; DB 2; Best Local Similarity 49.8%; Pred. No. 9.2e-23; Matches 607; Conservative 0; Mismatches 559; 1042 982 826 742 862 646 922 904 994 469 529 802

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Search completed: May 25, 2004, 06:30:47 Job time : 479 secs

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ALIGNMENTS

5239	
SI	BX325239 1042 bp mRNA linear EST 01-MAI-2003
NOITINI	BX325239 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
	Homo sapiens cDNA clone CSODJ010YL24 5-PRIME, mRNA sequence.
SSION	BX325239
NOIS	BX325239.1 GI:30309195
VORDS	EST.
CE	Homo sapiens (human)
RGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ERENCE	1 (bases 1 to 1042)
THORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
ITLE	Full-length cDNA libraries and normalization
DURNAL	Unpublished (2001)
MENT	Contact: Genoscope
	Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - France
	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
	Library was constructed by Life Technologies, a division Of
	Invitrogen. This sequence belongs to sequence cluster 5634.1 For
	more information about this cluster, see
	http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOAJO10DF12QF1
	&cluster=5634.f. Contact : Feng Liang Email : fliang@lifetech.com
	URL : http://fulllength.invitrogen.com/ InVitroGen_Corporation 1600
	Faraday Avenue Genoscope sequence ID : CSOAJ010DF12QF1.

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> BX325239 BX463023 BI761782 BX431866

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1042 1008 891 889

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848.4 767.4 698.2 647

Description

SUMMARIES

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Result No.

	N BX463023 Homo sapiens FETAL LIVER Homo sapiens CDNA CSODMO04YK02 5-PRIME, MRNA sequence. BX463023.1 GI:31025478 BX463023.1 GI:31025478 FX GET Sapiens (human) Homo sapiens (human) FX GET SAPIENS (human) FX GET SAPIENS (human)	REFERENCE 1 (bases 1 to 1008) AUTHORS 11, W.B., Gruber, C., Jessee, J. and Polayes, D. AUTHORS 11, W.B., Gruber, C., Jessee, J. and Polayes, D. TILE Full-length CDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT Genoscope - Centre National de Sequencage RP 191 91006 RVRY cedex - France	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invirrogen. This sequence belongs to sequence cluster 5634.f For more information about this cluster, see http://www.genoscope.cns.fr/	cgi-bin/cluster.cgi?seq=CSODM004BF01QP1&cluster=5634.f. Contact :	FEATURES Location/Qualifiers 11008 /organism="Homo sapiens" /mol type="mRNA"	/db_xref="taxon:9606" /clone="cSpW004xX02" /tissue_rEpETAL LIVER" /dev stage="fetal"	/clone_lib="Homo sapiens FETAL LIVER" /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double strand cDNA was digested with Not I and	cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	Query Match 45.6%; Score 767.4; DB 13; Length 1008; Best Local Similarity 93.4%; Pred. No. 1.2e-207; Matches 840; Conservative 31; Mismatches 19; Indels 9; Gaps 7;	Qy 1 AIGITIGCCAGGAIGICTGCAIGITCIGCIGTTAAIGGCTCTGGGAAAGACA 60	Qy 61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCGGGCCCTG-A 119	QY 120 CCAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACTTAC 179	Qy 180 CCATGCT-GAGAATCCTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCA	239
Location/Qualifiers 1. 1042 (organism="Homo sapiens" (organism="RNN" (db xref="taxon:9606" (ell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" (call type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED" (call line="Unitary" (ell line="Unitary" (coll line="Unitary" (coll line="Unitary" (coll line="Unitary" (coll line="Unitary" (coll line line "Unitary" (coll line "Unitary" (coll line "Unitary" (coll line "Unitary" (coll line "Uni	er. Five prime end enriched, double-strand cDMA was sted with Not I and cloned into the Not I and EcoR V of the pCMVSPORT 6 vector. Library was normalized. 50.4%; Score 848.4; DB 13; Length 1042; 98.1%; Pred. No. 8e-231;	CONSELVATIVE ATGITTGCCAGGATGICTGA ATGITTGCCAGGATGICTGA GCCTGTGGGTTCTCCCTGAI	ACTTACC ACTTACC	OY 181 CATGCTGACATCCTGACTGCTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 240	Oy 241 CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCTG 300	OY 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 360	dy 361 GGCCGGGCCAAIGFCTCATTACCCAGAGTCCTCCTACTACCGCTGTGTCTGTAAACAC 420	Qy 421 CCTTACACAGGTCCCAGCTGCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 480 Db 566 CCTTACACAGGTCCCAGCTGCTCCTGAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 625	OY 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC 540	Qy 541 CAGTICAAGGGAAAITCTGIGAAATAGGTTCTGATGACTGCTATGGCGATGGCTAC 600	Qy 601 TCTTACCGAGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 660 Db 746 TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 805	Qy 661 CACCTCTTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 720	QY 721 GGGGBACAC-AATTTCTGCAGAACCCAGATGCGGACGABAAGCCCTGGTGCTTATTAA 779 PN	780 AGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGA

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organism≈"Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Eukaryota; Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

LOF Prontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Contact: Kim YS

Contact: Kim YS

Contact: Nam YS

Cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1355 GGGGTGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGA 1414
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241 GAGAATCTATGGAGGCTTTAAGAGCACGGGGGGAAGCACCCATGGCAGGGGTCCCTCCA 300
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/clone lib="L17N670205n1"
/note="Organ: Liver, Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: Not1; The library was contributed by the Soares
                                                                                                                                                                                                              361 CCACCCCTGCTGGGGTGCTCACTGCCCACTGCACCGACCAAAAACAGACATAAAA
                                                                                                                                                                                                                                                                                                                                                                                         1176 GGAGAAGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTGCGCCACAATGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCCTCGCTGCCTCTGCTTCTCCATGCCCCCAGGCCCACTTCTGTGGTGGGGCGCTGAT
                                                                                               301 GICCICGCICICIGACCAICICCAIGCCCCAGGGCCACTICIGIGGGGGGGCGCTGAI
                                                                                                                                                                 1056 CCACCCTGCTGCTCACTGCTGCCCACTGCACATAAAACCAGACATCTAAA
                                                                                                                                                                                                                                                                                GGTGGTGCTAGGGGACCAGGACCTGAAGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGT
                                                                                                                                                                                                                                                                                                              421 GGTGGTGCTAGGGGACCAGGACCTGAAGAAGAAGAAGAATTCATGAGCAGAGCTTTAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1236 TGCATTGCTCAAGTTAAAGCCAGTGGATGGTCACTGTGCTCTAGAATCCAAATACGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1415 TIGCCAACACTTTGTGCAACTCCCGCCAACTCTATGACCACAT 1457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 İTGTCGACATİGGAGGGGGGGGTGGCTACTGTGTGTGCACAT 763
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L17N670205n1-4-F07"
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/mol_type="mRNA"|9606"
/dolone="cSoDW004YX02"
/tissue_type="FETAL LIVER"|
/dov stage="fetal"
/clone lib="Homo sapiens FETAL LIVER"
/clone lib="Homo sapiens FETAL LIVER"
/note="Organ: liber; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EconV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5634.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-cgoBAGO65ZHO5_CSO6184_1&cluster=5634.f.
Contact. Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAGO65ZHO5_CSO6184_1.
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BX431866
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              GGATTGGGGAAACACCAATTTCTGCAGAAAACCCAGATGCCGACGAAAAAGCCCTGGTGC 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo., 1 (bases 1 to 889)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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38.4%; Score 647; DB 13; Length 889;
Best Local Similarity 91.3%; Pred. No. 3e-173;
Matches 697; Conservative 0; Mismatches 65; Indels
                                                                       788
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                                                                                                  Homo sapiens (human)
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iaboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

1033 EST 30-JAN-2003 ö 913 157 914 AGATAGCAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGCACGGGGGAAGC 973 517 613 AAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTTGC 673 AAATGAATAGGACAGTCAACCAGCATGCGTGTTTTACTGGAACTCCCACCTCCTCTTGC 397 733 337 TCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAAGTTACCAATGACA 793 277 853 217 GCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGACCAGTTCAAGGGGA 553 AATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTACTCTTACCGAGGGA 457 97 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 663) Kim,N.S.; Hahn,Y.; Oh,J.H.; Lee,J.Y.; Ahn,H.Y.; Chu,M.Y.; Kim,M.R.Oh,K.J.; Cheong,J.E.; Sohn,H.Y.; Kim,J.M.; Park,H.S.; Kim,S. and 37 336 ICTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAAGTTACCAATGACA 116 AGGAAAGCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTG ACCCATGGCAGGCGTCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCC AGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATTGGGGAACACAATT 794 AGGIGAAAIGGGAAIACIGIGAIGICTCAGCCIGCICAGCCCAGGACGIIGCCIACCAAG 276 Acercadariocedaracrerorarioreredecercecedeceacerrecerace AGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTG 974 ACCCATGGCAGGCGTCCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCC AATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTACTCTTACCGAGGGA Gaps Oh.K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., K Kim, Y.S. 21C Fronter Korean EST Project 2001 Unpublished (2002) Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology S2 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea . 0 Length 576; CB162144 663 bp mRNA linear K-EST02222650 L17N670205nl Homo sapiens cDNA clone L17N670205nl-17-H10 5', mRNA sequence. Indels 1034 ACTICIGIGGGGGGGGCGCIGAICCACCCCTGCTGGG 1069 Score 572.8; DB 14; Pred. No. 3.8e-152; O; Mismatches 2; CB162144.1 GI:28148270 34.0%; larity 99.7%; Conservative Homo sapiens (human) Homo sapiens Similarity Query Match Best Local Simil Matches 574; C 854 554 516 614 456 674 734 ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION REFERENCE AUTHORS RESULT 6 CB162144 g d g g δ ò 셤 ò Dp ò g 8 G à Dp ò ò

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/lab_host="Top10F'"

/cone lib="L17N67020511"

/note="Organ: liver; Vector: pT7H3-Pac; Site_1: EcoRI;

Site_2: NotI; The library was contributed by the Soares

Site_2: NotI; The library was contributed by boared

laboratory and it was constructed as described by Bonaldo,

M.F. Lennon, G. and Soares, M.B. (1996), Genome Research

(9): 791-806. RNA was prepared from harvested cell
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AGENCOURT 12929103 NIH MGC_177 Mus musculus cDNA clone IMAGE:30310462 5', mRNA sequence.
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31.9%; Score 537; DB 14; L
Best Local Similarity 100.0%; Pred. No. 7.3e-142;
Matches 537; Conservative 0; Mismatches 0;
                                                                                                         /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="L17N670205n1-17-H10"
/sex="F"
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongeung@mail.kribb.re.kr
Plate: 17 row: H column: 10
High quality sequence stop: 663.
Location/Qualifiers
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/ Organism="Mus musculus"
/ Mol_Lype="mRAW"
/ Mol_Lype="mRAM"
/ Mol_Lype="mRAM"
/ Mol_Lype="mRAM"
/ Mol_Lype="mRAM"
/ Jab_host="DH10B (T1-phage-resistant)"
/ Loone lib=NNH MCC_177"
/ Lote="Organ: liver: Vector: pDNR-LIB; Site_1: Sfil
/ Ggccattaggcc); Site_2: Sfil (ggccgctcggcc); CDNA made
/ Ggccattaggcc); Site_2: Sfil (ggccgctcggcc); CDNA made
/ Syoligo-dT priming and directionally cloned. S' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGACAGGCAGAGAGGCGCGAATACGGCGGG-3' and
5'-AAGCAGTGGTATACAGGCAGACAGCAGACAGTGCGCGG-3' and
5'-AATCTAGAGGCGGGCGACAATACGCTGCGG-3' and
5'-AATCTAGAGGCGGGGCGACAATG-GT(30) NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

12. I (bases 1 to 736)

13. NIH-MGC http://mgc.nci.nih.gov/.

14. Unpublished (1999)

15. Contact: Robert Strausberg, Ph.D.

15. Email: cgapbs-r@mail.nih.gov

17. Tissue Procurement: Dr. Michael Brownstein Laboratory

18. CDNA Library Preparation: Michael Brownstein Laboratory

18. CDNA Library Preparation: Michael Brownstein Laboratory

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27.1%; Score 455.8; DB 14; Length 736;
Best Local Similarity 80.9%; Pred. No. 1.3e-118;
Matches 543; Conservative 0; Mismatches 127; Indels 1;
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đ	603	GCCACATCTCTGGCTGGGGGTGTTTCAGAAACAGG 662
ò	1374 AAAAGGGTCCC 1384	
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RESULT BE0320 LOCUS DEFINI ACCESS VERSIO KEYWOR SOURCE ORGA	8 18 100 100 N DS	2 bp mRNA linear EST 09-JUL-2000 cDNA 5', mRNA sequence.
REFER AUT	Mammalia; Eutheria; Cetartiodactyla; Suina; Su REFERENCE 1 (bases 1 to 592) AUTHORS Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cl Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Su. Quackenbush,J. and Keele,J.W.	ldae; Sus. no,J., White,J. ltana,R.,
TIT	TITLE Porcine gene discovery by n EST cluster assembly	normalized cDNA-library sequencing and
MED MED PU	BBK	8 (2002)
COMME	COMMENT Contact: Smith TPL USDA, ARS, US Meat Animal F PO Box 166, Clay Center, NE Tel-1402 752 4366	esearch Center : 68933-0166, USA
	Fmail: smith@email.marc.usc Single pass sequencing. Bas v0.980904.e. Vector identif and -minmach 12 options.	a gov ses called and alt trimmed with phred ied by cross_match with the -minscore 18
FEATU	FCK FRIMER FORWARD: A(BACKWARD: (BACKWARD: 69) Plate: 69 Seq primer	NT CG 12 IAAG.
	/organism="Sus scrofa" /organism="Sus scrofa" /doltype="mRNA" /tissus_type="pooled" /tab.host="DH10B" /lob="Lib="MARC IPIG" /note="Vector: pCNV SPORT6; /inbrary made from pooled tissuand and an ambrogal.	rofa" 123" ed" LPIG" N SPORT6; Site 1: Not1; Site 2: Sal1; pooled tissue from day 11, 13, 15, 20,
ORIGIN		
Que Bes Mat	Query Match Best Local Similarity 86.0%; Pred Matches 518; Conservative 0; M	Score 451.6; DB 10; Length 592; Pred. No. 1.8e-117; ; Mismatches 69; Indels 15; Gaps 1;
δλ	522	CACCIGIGCCIGICCCGACCAGIICAAGGGGAAAIITCIGIGAAAIAGGIICTGAIGACIG 581
qa	9	raagggagattetgtgaaataggttetgatgaetg 65
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Eutelecstomi;

Bukaryota, Metazoa, Chordata; Sciurognathi; Muridae; Musinae; Mus.

1(E 1 (bases 1 to 602)

DRS MIH-MGC http://mgc.nci.nih.gov/.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

The Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CONTACT: Robert Strausberg, Ph.D.

CONTACT: Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genemics, Inc.

Clone distribution: MGC Clone distribution information can be thus; //mage.llnl.gov.

Plate: LiAMN10867 row: a column: 17

High quality sequence stop: 785.

1.8802
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CTATGTTGGTGACGCCTACTCTTACCGAGGGGAAGTGAGTAAAACTGTCAACCAGCACCACC
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/strain="FVB/N"
/db_xref="taxon:10090"
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/clone lib="NCI CGAP Kidl4"
/note="Corgan: Kidney; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Corgan: Kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidiarectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library. |"
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Pred. No. 4e-116;
); Mismatches 158; Indels
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ON 602912432F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5053663 5',

MINA sequence.

ON BI148082.1 GI:14608083

S EST.

Mus musculus (house mouse)

ENGATYCEA, Metazoa, Chordata, Cramiata, Vertebrata, Buteleostomi;

Mus musculus (house mouse)

ENGATYCEA, Metazoa, Chordata, Cramiata, Vertebrata, Buteleostomi;

Mus musculus

ENGATYCEA, Metazoa, Chordata, Cramiata, Vertebrata, Buteleostomi;

Mus musculus

ENGATYCEA, Metazoa, Chordata, Cramiata, Vertebrata, Buteleostomi;

Musmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinee, Mus.

CE 11H-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL (bases 1 to 751)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

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Email: cgapbs-r@mail.nih.gov

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Context: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

Clone distribution: MGC clone distribution

Clone distribution: MGC clone distribution

Clone distribution: RGC clone distribution

High quality sequence stop: 747.

S High quality sequence stop: 747.

S High quality sequence stop: 747.
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/db.xerf="raxon:10090"
/clone="INAGE:5053663"
/lab_wost="NHIOB (TI phage-resistant)"
/clone lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pcWV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                           1061 COTGOTGGGTGCTCATGCTGCTGCACCGACATAAAAACCAGACATCTAAAAGGTGG
                                                                                                                                                                                                                                                                       361 CCTGCTGGTGCTCACTGCAGCCCACTGTACCGACATAAACACCCAAGCATCTAAAAGTTG
                                                                                                                                                                                                                                                                                                                                                                           1121 TGCTAGGGGACCAGGACCTGAAGAAAAATTTCATGAGCAGAGCTTTAGGGGTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                               421 TACTAGGGGATCAGGACCTGAAGAAGACAGAATCCCATGAACATTCAGGGTGGAAA
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/organism="Mus_musculus"
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/strain="FVB/N"
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Unpublished (1996)

Conteact: Marra M/Mouse EST Project
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Mus musculus
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba; T., Lacy, M., Le, M., Martin, J., Morris, M.,
Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           701 ATGCTGAAACCCATGGGATTGGGGAACACACAATTTCTGCAGAAACCCAGATGCGGACGAAA 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATTCGGAAGAGGCACGGGATCGCAGACCATCTGCAGAAACCCAGATGGAGACCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ARCCCTGGTGTTTCGTCAAGGTGAACAGTGAAGGTGAAATGGGAATACTGTGATGAATGTCA
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26.0%; Score 437.8; DB 9; Length 67.
Best Local Similarity 78.2%; Pred. No. 1.8e-113;
Matches 526; Conservative 0; Mismatches 147; Indels
                               AA217892.1 GI:1826875
EST.
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-ii37h03.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
musculus cDNA clone IMAGE:5944156 5' similar to TR:Q14520 Q14520
HGF ACTIVATOR LIKE PROTEIN. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                               183 TGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAACCC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 CTGTGAACACGGGGGGACTGTATCATCAGGGGGATACCTTCAGTTGCAGCTGCCCAGC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 TCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTGTAAACACCCC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAGAA 482
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 570)
                                                                                                                                                                                          CTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGACCA 122
                                                                                                                                                                                                                      CATTGGGCTCTCACTGATGTCCTTCATTGCGCCCCCAGACCCAGATTGGACCCCCGATGA 121
                                                                                                                                                                                                                                                                                     123 GTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACCCA 182
                                                                                                                                                                                                                                                                                                                                 122 CTATTACTACAGCTATGAGCAGTCCAGCCCAGACGAAGACCCCAGTGTCACGCAGACCAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTGGC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 cécerrérégégégégegérégégégénegadaaabaaagagagagadaaccargigi 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 IGGCGGAGTCTGTTCCCGACACAGAGATCCAGGTTTACCTGTGCCTGTCCAGACCA 535
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                                                                                              4 TTTGCCAGGATGTCTGATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACAGC- 62
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Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                          182 cccrigadaaccccgacrggracr----argaagacgargarccargccagrccaaccc
                                                     Gaps
                                                     10;
     DB 12; Length 751;
Query Match 25.9%; Score 435.4; DB 12; Length Best Local Similarity 78.0%; Pred. No. 9.2e-113; Matches 589; Conservative 0; Mismatches 156; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 617-495-1812
Fax: 617-495-1812
Fax: 617-495-8537, harvard.edu
Libral: dealton@biohp, harvard.edu
Libral: was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:2007028 This sequence now available from the INAGE consortium,
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ilj7103.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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/n.MMSI"
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25:9%; Score 435.2; DB 12; Length 570;
Best Local Similarity 85.4%; Pred. No. 8.8e-113;
Matches 485; Conservative 0; Mismatches 83; Indels 0;
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 TATGTGAAGACTGTATGTTTGCCCAGCGACCCCTTTCCCTCTGGAACTGAGTGCCACATC 242
                                        243 TCTGGCTGGGGTGTTACAGAAAAGGGGAAGGGTCCCGCCAGCTCCTGGATGCTAAAGTC
                                                                                                                          363 AGTATGATTTGTGCGGGGAACCTTCAGAAGCCCGGATCAGACACCTGCCAGGGTGACTTC
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p mRNA linear BST 12-JAN-2001 musculus cDNA clone IMAGE:4241642 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 929)

11 HMG http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999) 929 bp 602113411F1 NCI CGAP_Kid14 Mus m 5., mRNA sequence.
BF788188. GI:12093224 Mus musculus (house mouse) Mus musculus ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 13 BF788188

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/clone lib="w.C1 CGAP Kid14"
/note="Crgan: kidney; Vector: pCMV.SPORT6; Site_1: Not1;
Site_2: SAll; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |" Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9858 row: e column: 03
High quality sequence stop: 686. /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" FEATURES

Gaps 9 Score 416.4; DB 10; Length 929; Pred. No. 2.9e-107;); Mismatches 162; Indels 6; ; 0 Query Match 24.7%; Best Local Similarity 75.9%; Matches 529; Conservative

ORIGIN

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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 665)
Piao, Y., Ko, N. T., Lim, M. K. and Ko, M. S. H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method CF169114 665 bp mRNA linear BST 25-JUL-2003 B0809C08-5 NIA Mouse Newborn Kidney CDNA Library (Long 1) Mus musculus CDNA clone NIA:B0809C08 IMAGE:30468319 5', mRNA sequence. CP169114.1 GI:33278663 ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE

RESULT 14 CF169114

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Contact: Dawood B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Genome Res. 11 (9), 1553-1558 (2001) 21429098 11544199 MEDLINE PUBMED COMMENT JOURNAL

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ద ð g ò à d a δ ठ ò 360 370 420 137 GACTATTACTACAGCTATGAGCAGTCCAGCCCAGACGAAGACCCCAGTGTCACGCAGGACC 196 181 CATGCTGAGAATCCTGACTGCTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 240 197 ACCCCTGAGAACCCCGACTGGTACT-----ATGAAGACGATGATCCATGCCAGTCCAAC 250 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120 77 GTCATTGGGCTCTCACTGATGTCCTTCATTGCGCCCCCAGACCCCAGATTGGACCCCCGAT 136 121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAAGAACACCAGTAGCACTTACC 180 241 CCCTGTGAACACGGTGGGGACTGCCTCCATGGGAGCACCTTCACATGCAGCTGCCTG 300 1 ATGITTGCCAGGATGTCTGCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60 17 ATATITGICAGGATGITGGTGTTCCGTGTCCTGCTGCTAATCGCCCTGGTGGGAAGTCA 76 clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long 311 GCCCCCTTCTCGGGGGCCGGTGCCAGACTGCACAAAACAAGTGCAAGGACAACCCATGT GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 361 GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC 9 23.7%; Score 399.4; DB 14; Length 665; 76.8%; Pred. No. 1.7e-102; ive 0; Mismatches 146; Indels 6; /organism="Mus musculus"
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CCTTACACAGGTCCCAGCTGCTCCCAGTTCCTGTATGCAGGCCAAACCCCTGCCAG

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SM Muss musculus (Mouse Mouse)

Bukaryota Metazoa Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musn.

1 (Dasea 1 to 791)

SNIH-Moc http://mgc.nci.nih.gov/.

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: capbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CONDA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

http://image.llnl.gov

Plate: LiAMIl328 row a column: 12

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/note="Organ: Ilver, Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
/Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library." BI332440 791 bp mRNA linear BST 30-JUL-2001 602980841F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5133587 5', mRNA sequence.
BI332440 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCCAGACTGGACCCCTGAC 120 180 600 CCTIACACGGGACCAGACTGCTCCAAAGTGCTTCCGGCATGCAGGCCAAACCCCTGCCAG 490 82 9 drcarrigadoricricacridaridatecricaccococaga cocagarraga occocaga r 121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACACTTACC 1 ATGITIGCCAGGAIGTCIGATCICCAIGITCIGCTGTTAATGGCTCTGGTGGGAAAGACA CAGITICAAGGGGAAATICIGIAAATAGGITICIGAIGACIGCIAIGITIGGCGAIGGCIAC 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC 652 601 TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGA 1, 23.6%; Score 396.4; DB 12; Length 791; llarity 75.6%; Pred. No. 1.4e-101; Conservative 0; Mismatches 161; Indels 7; EST. Mus musculus (house mouse) BI332440.1 GI:15017097 Local Similarity es 520; Conserv 23 61 83 541 Query Match 431 VERSION KEYWORDS SOURCE ORGANISM Best Loca Matches DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 15 BI332440 LOCUS ACCESSION FEATURES ORIGIN

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600 CTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCAGCATCTTACTGGAACTC 659
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Sequence 39, Appl
Patent No. 5344777
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Sequence 14, App
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Sequence 2, Ay
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Sequence 60, 7
Sequence 2, Ag
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Sequence 44,
Sequence 46,
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Sequence 1, 1
Sequence 1, 1
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Sequence 58,
Patent No. 52
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Sequence 9,
Sequence 9,
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-448-937A-3
US-08-427-640-1
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US-09-553-498-9
US-09-513-498-9
US-08-811-949-48
US-08-811-949-48
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US-08-286-740-1
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US-08-448-937A-2
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Gapop 10.0 , Gapext 1.0
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08-558-269 09-410-882	US-08-811-949-64 US-08-811-949-66	-811-949	ກຸກ	US-08-811-949-62	5200340~1	۲.	'n	-949-	-119-512-	8-015	US-08-488-015B-25	5200340-5	5185259-2	US-09-518-046-3
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Sequence 14, Application US/08148910

Sequence 14, Application US/08148910

Patent NO. 5466593

GENERAL INFORMATION:

APPLICANT: Takeshi SHIMOMURA et al.

APPLICANT: Takeshi SHIMOMURA et al.

TITLE OF INVENTION: NO. 546659381 Protein and Gene Encoding Said Protein

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoch, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

STREET: D.C.

COUNTRY: U.S.A.
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LIBRARY: Pre-made Lambda phage Library,
LIBRARY: human liver(49, male) cDNA Library (Stratagene)
                                                                                                                                                                                                                                                                                                                                                                                                                             CIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 Kb Storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/148,910
FILING DATE: No. 5466593ember 5, 1993
CLASSIFICATION: 435
PLIOR APPLICATION OPTA:
APPLICATION NUMBER: FILING DATE:
ATTORNEY/ASBT INFORMATION:
NAME: WALYEN CHECK, JT.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 202-371-8856
ALIGNMENTS
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SEQUENCE CHARACTERISTICS:
LENGTH: 2033 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE: ORGANISM: human
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TRY: U.S.A.
20005
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Thu May

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1738 AACANGCTCTGTGCCGGCTACTT---CGACTGCAAGTCCGACGCCTGCCAGGGGGACTCA 1794
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human liver(49, male) cDNA Library (Stratagene)
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Pred. No. 4.8e-25;
0; Mismatches 559;
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US-08-448-937A-14
US-08-448-937A-14
Sequence 14, Application US/08448937A
PATENT NO. 5677164
GENERAL INFORMATION:
APPLICANT: TARSEAL SHIMOMURA et al.
TITLE OF INVENTION: NO. 5677164el Protein and
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Mashington
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FILING DATE: May 24, 1995
CLASSIFICATION: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: No. 5677164ember 5
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1642 AATTGGATCAAAGCCACCAT 1661
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MEDIUM TYPE: Diskette, 5.25 ir
MEDIUM TYPE: 500 KD Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPOFFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warren M. Cheek, Jr.
REGISTRATION UNDBER: 33.367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 202-371-8856
TELEPAX: 202-371-8856
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LENGTH: 2033 base pairs
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Matches 607; Conservative
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CURRENT APPLICATION DATA:
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STRANDEDNESS: double
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ORIGINAL SOURCE:
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Thu May 2/ 10:53:53 2004

CIAGGGGACCAGGACCTGAAGAAAGAAGTTTCATGAGCAGAGCTTTAGGGTGGAGAAG 1661 1642 AATTGGATCAAAGCCACCAT 3; INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
LENGTH: nucleic acid
STRANDEDNESS: double 1588 GGCCTGGAGTGTGGGlinear MOLECULE TYPE: CI ORIGINAL SOURCE: ORGANISM: human IMMEDIATE SOURCE: LIBRARY: US-08-148-910-3 1009 1123 261 g ò g ò ઠે 셤 ઠે 1677 1854 1498 charicceácricadaaaaaaaaaaaaccecricacacacaccicecaarricaracaaccic 1557 1558 Archeccieccedeccedecadeaceciricecedadacaeaaadreceadarreceded 1617 1354 TGGGG-----TGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC 1407 .678 ceceridarededadeacaadridedadadedecreadarieraededededadararedededed 1737 AACATGCTCTGTGCCGGCTACTT---CGACTGCAAGTCCGACGCCTGCCAGGGGGACTCA 1794 GGAGGCCCCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGG 1587 GIGCIAGGGGACCAGGACCTGAAGAAAGAATTICAIGAGCAGAGCITIAGGGIGGAG 1179 1381 gráchadaccasocarrenteaaccacacacacarcarcacácacarredecanteas 1440 AAGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCACAATGATATTGCA 1239 1441 AAGTACATCCCGTACACCCTGTACTCGGTGTTCAACCCCCAGCGACCAC---GACCTCGTC 1497 1240 TIGCICAAGIIAAAGCCAGIGGAIGGICACIGIGCICIAGAAICCAAAIACGIGAAGACI 1299 1300 GIGIGCITGCCIGAT -----GGGICCITICCCICIGGGAGIGAGIGCCACAICICGGC 1353 1006 CCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGCGCTGATCCACCCTGC 1065 TOGGTGCTCACTGCCCACTGCACCGACATAAAAACCAGACATCTAA-----AGGTG 1119 1099 idcanicce-----caccadatecanercaccedatecededice -- Gerigacia cententa e a caractera de contrator de caractera de contrator de contr 1042 redréchacer---edrahacalcacecercrecreseariaciececeresaesec 1098 GGAGGCTTTAAGAGCACGGCGGCAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTG 1005 CCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAGGAAGATCAAGAGAATCTAT 945 705 TGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCC 825 826 IGCTCAGCCCAGGACGTIGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCTAAGCTT 885 585 861 645 921 cheaccheeaachceanchachchachaeaachecheaachceardaacacecee GGGGGGCCCTGGCGAGAAGAACGGCGTGGCTTACCTCTACGGCATCATGGCTGG 1618 receserrecarrecareacereaceceraricacircarciaciacecarecia 1468 AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT 982 ecccrecradaccradecccccaraccradideceaaricceaareaceageccc ścinecciaccaeecrinecriesaceecriciecaacarcaeccieardaececnecine GTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGC 862 Traddanacadcacraagraccaraaccaaccaccaccrcaaccrcaagccrcaagcraacrag CTITACTGGAACTCCCACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCT GAAACCCATGGGATTGGGGAACACACAATTTCTGCAGAAACCCCAGATGCGGACGAAAAGCCC GCCTGTCCCGACCAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGA 1738 1528 1795 988 1120 1180 1263 1066 946 802 646 994 586 922 706 셤 ò g Д à δ 셤 ò ò 셤 à DP 상염 à gg 8 8 8 Db ò dd 8686 8 Op d

1122 1182 9 260 1855 dereacdecricededececrecacadecededecereracacececeredecearcharere 1914 ----AAGAGGCCAGGGGTCTACACCCAAGTTACCAAATTCCTG 1641 SHIMOMURA et al. No. 5466593el Protein and Gene Encoding Said Protein dricariencedecedecatrica de la contra dela contra de la contra de la contra de la contra de la contra de la contra dela contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra dela contra de la contra del contra della contr CTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGCGCTGATCCACCCCTGCTGG GTGCTCACTGCTGCCCACTGCACCGACATAAAAACCAGACA-----TCTAAAAGGTGGTG 30; Length 970; Indels Pre-made Lambda phage Library, human liver cDNA Library (Stratagene) Query Match
5.7%; Score 96.2; DB 1; I
Best Local Similarity 53.0%; Pred. No. 8.8e-19;
Matches 359; Conservative 0; Mismatches 288; RESULT 3
US-08-148-910-3
US-08-148-910-3
; Sequence 3, Application US/08148910
; Patent No. 5466593
; GENERAL INFORMATION:
; APPLICANT: Takeshi SHIMOMURA et al.
; TITLE OF INVENTION: No. 5466593el Protein an.
; NUMBER OF ENCUENCES: 14
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
CCUNTEY: U.S.A COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 KD Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Ms-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION NUMBER: US/08/148,910
FILING DATE: No. 5466593ember 5, 199
CLASSIPICATION NUMBER: TAFORMATION:
APPLICATION NUMBER:
FILING DATE: ATORNEY, AGENT INFORMATION:
NAME: WARTEN M. CHEEK, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-371-8856

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Sequence 3, Application US/08448937A

| Sequence 3, Application US/08448937A
| Patent No. 5677164
| Patent No. 5677164
| Patent No. 56771640|
| APPLICANT: Takeshi SHIMOMURA et al.
| TITLE OF INVENTION: No. 56771640| Protein and Gene Encoding Said Protein NUMBER OF SEQUENCES: 14
| CORRESPONDENCES: 14
| CORRESPONDENCES: 14
| CORRESPONDENCES: 14
| CORRESPONDENCES: 15
| COUNTRY: Washington STATE: D.C. COUNTRY: U.S.A.
| STATE: D.C. COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, MEDIUM TYPE: Diskette, 5.25 inch, MEDIUM TYPE: IBM Compatible OPERATING SYSTEM: MS-DOS SOFFWARE: WS-DOS SYSTEM: MS-DOS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GG-----TGTTACAGAAACAGGAAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAG 1410
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CIGGGCCAGCACTICTICAACCGCACGACGACGTGACGCAGACCTICGGCATCGAGAAG 380
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APPLICATION NUMBER: US/08/448,937A
FILING DATE: MAY 24, 1995
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 56/7164ember 5, 1993
ATTOCNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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Length 970;
5.7%; Score 96.2; DB 1;
53.0%; Pred. No. 8.8e-19;
tive 0; Mismatches 288;
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US-08-427-640-1
; Sequence 1, Application US/08427640
; Parent No. 5658788
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                                                                                                                                              Conservative
                                                                                 Similarity
                                                                                 Best Local Simi
Matches 359;
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male)

LIBRARY: Pre-made Lambda phage Library, human liver LIBRARY: cDNA Library (Stratagene)

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

linear

ORGANISM: huma IMMEDIATE SOURCE: TOPOLOGY: line MOLECULE TYPE: ORIGINAL SOURCE:

; US-08-448-937A-3

Disor US-08-427-640-5
US-08-427-640-5
Sequence 5, Application US/08427640
Patent No. 5558788
GENERAL INFORMATION:
APPLICANT: Berg et al.
APPLICANT: Berg et al.
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Lilly Corporate Center
STREET: Lilly Corporate Center
STREET: IN.
COUNTRY: U.S.A. 1087 1141 1142 AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201 TTCCCT------CTGGGAGTGAGTGCCACATCTCTGGCTGGGTGTTACAGAAA 1369 1202 ACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261 451 corcecciónide cenadado de construcción de la constr 452 gerrechaganganirecaceeeeeeeaeeiganeeriganerigagaeenganeeraheee 392 Agcegrichereceseseseracicaleacitériseriseriseristréfecesécéser 1088 GCACCGA-----CATAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 512 restroctingeceangandenschaartricaactichaaaaracartetocaraaggaar 572 TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 1028 AGGGCCACTICTGTGGTGGGCGCTGATCCACCCCTGCTGGTGCTCACTGCTGCTGCCACT 1595 AGTGTGGGAAGAGG-----CCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGA 4.5%; Score 75.4; DB 1; Length 1065; 50.8%; Pred. No. 1.7e-12; ive 0; Mismatches 286; Indels 45 Mb storage 1.0 ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft OPERATING SISIEM: MACTOSOFT WATG SOFTWARE: Microsoft Ward CURRENT APPLICATION DATA: PILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/689,410 FILING DATE: 22 APRIL 1991 FILING DATE: 22 APRIL 1991 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1065 Dase pairs 1046 Trcgracacar 1058 Matches 342; Conservative LENGTH: 1065 base pai TYPE: nucleic acid STRANDEDNESS: double 1649 TCAAAGCCACCAT Similarity TOPOLOGY: 1i: MOLECULE TYPE: ; US-08-427-640-5 Query Match Best Local ð g g g 유 g δ ò ò à ਨੇ 임 음 ઠે 8 g APPLICANT: Berg et al.
TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN. 1087 1321 CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369 1430 GCAACTCCCGCCAACTCTATGACCACATGATTGATGACAGTATGATCTGTGCAGGAAATC 1489 1141 1201 ------GCAAGACACCTGCCAGGGTGACTCTGGAGGCC 1534 CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG 1594 .202 ACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261 451 511 ecacarcacaacarriacriaacagaacagicacceacaacaiecreierereceaeaea 865 572 regair-----daidacaerraegacahadaearridegeridergeadergaarregarr CTCGGAGCGGCGCCCCAGGCAACTTGCACGACGCCTGCCAGGGCGATTCGGGAGGCC 1028 AGGGCCACTICTGTGGTGGGGGGCTGATCCACCCCTGCTGGTGCTCACTGCTGCCCACT 392 Adcidentécrique de des de la contra dela contra de la contra de la contra de la contra de la contra dela contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra dela contra de la contra dela contra del la contr 1088 GCACCGA-----CATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 452 GCTTCCAGGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATACCGGG 1142 AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 512 TGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATTGTCCATAAGGAAT 626 cercceciráriocechada a carachece a contratar de contrata de co CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT crccrrrcrarricegageedergaaggecrcargreagactearccarccaecer Gaps 45; Length 1065; Score 75.4; DB 1; Length 1 Pred. No. 1.7e-12; 0; Mismatches 286; Indels COUNTY,
ZIP: 46285
COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPITER: Macintosh
Macintosh
Macintosh SOFTWARE: Microsoft Word CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/427,640 FILING DATE:
CLASSIFICATION 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 07/689,410
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double Query Match Best Local Similarity 50.8%; Matches 342; Conservative 1322 TTCCCT------1490 TICAGAAACCIGG-; TOPOLOGY: Linear; MOLECULE TYPE: DNA US-08-427-640-1 U.S.A. GENERAL INFORMATION: COUNTRY: 1370 1535 746 908

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1370 CAGGAAAAGGGICCCGCCAGCICCTGGATGCCAAAGICAAGCTGATTGCCAACACTTTGI
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Pred. No. 1.8e-12;
0; Mismatches 286; Indels
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; Sequence 9, Application US/09553498
; Patent No. 630961
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Josep
; APPLICANT: Schaeffner, Josep
; PTILE OF INVENTION: Process for the production of natural prints of INVENTION: Process for the production of CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT APPLICATION NUMBER: EP99107412.1
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-64-26
; NUMBER OF SEQ ID NOS: 10
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US-09-553-498-9
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Sequence 3, Application US/08427640

Batent NO. 5658788

GENERAL INFORMATION:
APPLICANT: Barg et al.
TILLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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tive 0; Mismatches 286;
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SULP: 46285.

ZIP: 46285.

CAMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb sto
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,640
FILING DATE:
CLASSIFICATION 10ATA:
APPLICATION NUMBER: 07/689,410
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
CHARADEDINESS: Gouble
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STATE: IN.
ZIP: 46285
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
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APPLICANT: SAITO, YOSHHWASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: SASAKI, HITOSHI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUSE
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE: ADDRESS:
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; Sequence 48, Application US/08811949
; Patent No. S840533
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; NAME/KEY: CDS
; LOCATION: (1)..(1137)
US-09-618-869-9
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                                                                                     1088 GCACCGA-----CATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTGA 1141
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    1028 AGGGCCACTICTGTGGGGGGGGGGGTGATGCACCCCTGCTGGTGGTGCTGCTGCTGCTGCTGT 1087
                                                                                                                                                                      1142 AGAAAGAAGAATTICATGAGCAGAGCTTTAGGGTGGAGAGATATTCAAGTACAGCCACT 1201
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                                                                                                                                                                                                                                                                                                                                             1262 ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321
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                                                                                                                               521 GCTTCCAGGAGGTTTCCGCCCCACCAGGTGATCTTGGGCAGAACATÀCCGGG 580
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APPLICANT: Rubosius, Dorthee
APPLICANT: Rubolph, Rainer
APPLICANT: Schaeffner, Josef
APPLICANT: Schaeffner, Josef
APPLICANT: Schwarz, Bliabeth
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED
TITLE OF INVENTION: BECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
TITLE OF INVENTION: CHAPERONES
FILE OF INVENTION: CHAPERONES
FILE OF INVENTION: CHAPERONES
FILE OF THE SPORT OF 19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR APPLICATION NUMBER: E999114811.5
FRICK APPLICATION NUMBER: E9907-29
NUMBER OF SEQ ID NOS: 10
                                       581 TGGTCCCTGGCGAGGAGGAGGAGAATTTGAAGTCGAAAATACATTGTCCATAAGGAAT
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Patent No. 6455279
GENERAL INFORMATION:
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ORGANISM: Escherichia coli
FEATURE:
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LENGTH: 1137
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Query Match
4.5%; Score 75.4; DB 4; Length 1137;
Best Local Similarity 50.8%; Pred. No. 1.8e-12;
Matches 342; Conservative 0; Mismatches 286; Indels 45; Gaps
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1142 AGAAAGAAGTITCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCACT 1201
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                                                                                    1172 cechiegreneheneakadandekesentekerringgredekentekeridekeketidek 1231
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Tissue Plasminogen Activator
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MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: VSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 7841-062
REFERENCE/DOCKET NUMBER: 7841-062
TELEPAX: (416) 364-7311
TELEPAX: (416) 364-7311
TELEPAX: (416) 364-7311
TELEPAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 1955 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle
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Best Local Similarity 50.8%; Pred. No. 2.4e-12;
Matches 342; Conservative 0; Mismatches 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-883-795A-39
is Sequence 39, Application US/08883795A
is Patent No. 5985607
is GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
ITILE OF INVENTION: Recombinant DNA
TITLE OF INVENTION: Vectors for Tis
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSES: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                    TCAAAGCCACCAT 1661
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US-08-883-795A-39
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STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
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50.8%; Pred. No. 1.9e-12;
tive 0; Mismatches 286; Indels
I: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
ARLINGTON
                                                                                                                                                                                                                                                                                                            MEDIUM TYEE: FLOPDY glash

COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/NN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MR 1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REPERBENCE/DOCKET NUMBER: 18-966-0
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-220
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 13.14 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: DNA (genomic)
PEATURE:
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Best Local Similarity 50.8
Matches 342; Conservative
                                                                                                                              STATE: VA-
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
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LOCATION: 1..1311
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US-09-703-695A-3
i Sequence 3, Application US/09703695A
j Sequence 3, Application US/09703695A
j Patent No. 6593097
j GENERAL INFORMATION:
j APPLICANT: Xu, Yuan
j TILE REFERENCE: P1788R1
j CURRENT APPLICATION NUMBER:
CURRENT PILING DATE: 200-11-01
j PRIOR APPLICATION NUMBER: US 60/163,607
j PRIOR PELING DATE: 1999-11-04
j NUMBER OF SEQ ID NOS: 4
j SEQ ID NO 3
j LENGTH: 2544
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larity 50.8%; Pred. No. 2.8e-12;
Conservative 0; Mismatches 286;
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                                                    TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCTGCAGCTGAAATCGGATT 1336
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1028 AGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTCTGCGGCCCACT
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PAPPLICATION NO. 5344773

APPLICATION OF THE FIGURO, NANCY, REDDY, VERMURI B.;

LEMONIT, JEFFREY F. DACKCWSKI, WILLIAM, DOUGLAS, RICHARD;

COLE, EDWARD S., PURCELL JR., RICHARD D., LAU, DAVID TAI-YUI

TITLE OF INVENTION HUMAN UTBRINE TISSUE PLASMINOGEN

ACTIVATOR PRODUCED BY RECOMBIANT DNA

NUMBER OF SEQUENCES: 6

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/O7/782,686

FILING DATE: 01-OCT-1985

PRIOR DATE: 01-OCT-1985

PRIOR DATE: 01-OCT-1985

PRIOR DATE: 01-OCT-1985

PRIOR DATE: 01-OCT-1985
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                                                                                                                                                                                                                                             Score 75.4; DB 1; 1
Pred. No. 5e-12;
0; Mismatches 286;
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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GENERAL INFORMATION:
APPLICANT: GENENTECH, INC.
TITLE OF INVENTION: METHOD FOR SEI
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      4.5%;
50.8%;
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                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.8
Matches 342; Conservative
                 i LENGIR: Joo LOCAL
FIRANDENESS: double
STRANDENESS: double
J. TOPOLOGY: linear
US-08-286-740-1
        7360 bases
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PCT-US95-09576-1
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                                                                                                                                                              1332 CGTCCCGCTGTGCCCCAGGAGAGCAGCGTCGCACTGTGTGCCTTCCCCCGGCGGACC
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Fatent No. 5561053
GENERAL INFORMATION:
FAPLICANT: Crowley, Craig W.
TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
TITLE OF INVENTION: HOST CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STREET: ADDRESSEE: California Francisco
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datin (Genentech)
CURRENT APPLICATION DATE:
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
FILING DATE: 04-AUG-1994
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/922-9881
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: Lee, Wendy M.
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-286-740-1
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1595 AGTGTGGGAAGAGG-----CCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGA 1648
                         Search completed: May 25, 2004, 10:46:15
Job time : 98.5 secs
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Best Local Similarity 50.8%; Pred. No. 5e-12;
Matches 342; Conservative 0; Mismatches 286; Indels
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09576
FILING DATE: 05-8043-1994
ATTORNEY/AGENT INFORMATION:
NAME: 160, Wendy M:
REGESTRATION NUMBER: 798PCT
FILING DATE: 05-804-1994
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7360 bases
TELER: nucleic acid
STRANDEDNESS: double
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Run on: May 25, 2004, 09:00:39 ; Search time 528:5 Seconds

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Title: (186-09-912-559-1)

Sequence: 1683
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Sequence: 1683
Sequence: 2553838 seqs, 2272363821 residues

Foral number of hits satisfying chosen parameters: 5907676
Minimum DB seq length: 0
Maximum Match 104
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Post-processing: Minimum Match 104
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result	ı	Query				
NO	. Score	Match	Match Length DB	<u>B</u>	QI	Description
:	1 1683	100.0	1683	. 6	US-09-912-559-1	Sequence 1, Appli
	2 1683	100.0	1683	16	US-10-391-215-1	Sequence 1, Appli
	3 1683	100.0	3008	σ	US-09-880-107-1668	Sequence 1668, Ap
	4 1681.4	99.9	1683	16	US-10-391-215-2	Sequence 2, Appli
	5 1681.4	6.66		16	US-10-391-215-3	Sequence 3, Appli
	6 1679.8	99.8	1683	σ	US-09-912-559-2	Sequence 2, Appli
	7 1679.8			16	US-10-391-215-4	Sequence 4, Appli
	368.4			10	US-09-918-995-8242	Sequence 8242, Ap
	9 262.4	15.6		13	US-10-425-000-17	Sequence 17, Appl
O	0 120,2			თ	US-09-864-761-11164	Sequence 11164, A
٦	1 117.6			σ	US-09-954-456-552	Sequence 552, App
Н	2 117.6			ഗ	US-09-880-107-1612	Sequence 1612, Ap
Ö	3 117			σ	US-09-864-761-27791	Sequence 27791, A
ਜ	4 93.2	S. 53	1302	13	US-10-087-192-590	Sequence 590, App

Sequence 10, Appl	'n	Ŋ		Sequence 25, Appl	N	w	ഗ	-	Sequence 5, Appli	Seguence 540, App	Sequence 540, App	Sequence 3, Appli	Sequence 144, App	2 Sequence	m	Φ	•	Sequence 7, Appli	٠.		Sequence 2, Appli	m	ednence	equence	equence	ഗ	Sequence 133.	Sequence 14,		and tot open
US-10-665-216-10	US-09-969-271-6	S-10-41	10-411-0	7-4	0	0-342-88	\circ	10-193-6	1-969-27	US-10-342	US-10-172-118-	US-10-443			3 US-10-027-632-1	6 US-10-027-632-17	-60-SD	US-09-987-455	US-09-987-455-	0-60-SD	US-10-401-077-	1-792-3	US-10-004-113	US-10-004-	US-10-152-3	US-09-898-837A-1	ns	US-09-898-8	US-09-898-837A-17	
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ALIGNMENTS

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WESOUL INCORMATION:
Sequence 1, Application US/09912559
PRECED NO. US20020142316A1
GENERAL INCORMATION:
APPLICANT: STOERN; HANS-ARNOLD
APPLICANT: STOERN; HANS-ARNOLD
APPLICANT: STOERN; HANS-ARNOLD
APPLICANT: LANG, WIEGAND
APPLICANT: LANG, WIEGAND
APPLICANT: MERCRET
APPLICANT: WERENCE, ANNERTE
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 US-10-391-215-1
Sequence 1, Application US/10391215
Sequence 1, Application US/10391215
Publication No. US20040009543A1
GENERAL INFORMATION:
APPLICANT: MIEDER, STEFAN
APPLICANT: MIEDER, AUGREN
APPLICANT: MEDERMANN, CHRISTIAN JOSEF
APPLICANT: MEDERMANN, CHRISTIAN JOSEF
APPLICANT: MEDERMANN, CHRISTIAN JOSEF
APPLICANT: PEUSNER, ANNETTE
APPLICANT: STOERR, ANNETTE
APPLICANT: STOERR, HANS-ARNOLD
APPLICANT: STOERR, HANS-ARNOLD
APPLICANT: MEDERAM, VOLKER
APPLICANT: MEDERAM, VOLKER
APPLICANT: MEDERAM, VOLKER
APPLICANT: MARBURG I MUTANT OF FACTOR FOR ARTERIAL THROMBOSIS
FILE REFRERENCE: 06478-1457-01
CURRENT APPLICATION NUMBER: US/10/391,215
CURRENT APPLICATION NUMBER: US/10/391,215
CURRENT PELING DATE: 2003-07-26
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 100 50 040-4
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR FILING DATE: 2000-10-12

	1021 ATGCCCAGGGCALTTCTGTGGTGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	Oy 1141 AAGAAGAAGTITICATGAGGGGTGGAGGAGAAGATATTCAAGTACGCAC 1200	1261 GATGGTCACTGTGTCCAATACGTGAAGACTGTGTGTGTGT	Db 1321 TTTCCTCTTGGAAGTGCACATCTCTGGCTGGTTACAGAAACAGGAAAAGGG 1380 Qy 1381 TCCGGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 1440 Db 1381 TCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACTTTGTGCAACTCCCGC 1440	1441	1501 GGCGAGGACCCCGGCGGGGGGGGGGGGGGGGGGGGGG	1561 TACTACGGCTTATGGGATAGTGAGCTGGGGCCTGGAGTGTGGGAAGAGGCCAGGGGTCTACGGATCTACGGATCTACGGATCTACGGAGAGTGTGAGAGAGA	Db 1621 ACCCAAGTTACCAAATTCTGAATGAATCAAAAGCCACCATCAAAAGTGAAAGTGGCTTC 1680 Qy 1681 TAA 1683	 1681 TAA	RESULT 3 US-09-880-107-1668 Sequence 1668 Application US/09880107 Sequence 1668 Application US/09880107) GENERAL INFORMATION: OCKLEY, JOSEPH G. ; APPLICANT: Horne, Darci T. ; APPLICANT: Horne, Joseph G. ; APPLICANT: Scherf Inc.	APPLICANT: Gene Logic, Inc. ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer ; FILE REPERENCE: 44921-5028-00 ; FILE REPERENCE: 44921-5028-00 ; FILE REPERENCE: 44921-5028-00	CURRENT AFFLIATION WORDER: US/03/00/10/ CURRENT FILING DATE: 2001-06-14 ; PRIOR APPLICATION NUMBER: US 60/211,379 ; PRIOR FILING DATE: 2000-06-14 ; PRIOR APPLICATION NUMBER: US 60/237,054
	10, Indels TRAATGGCTCTGG	Qy 61 GCCTGTGGGGTTCTCCCTGATGTCTTATTGGAAAGCCTGGACCCCTGGACCCCTGAC 120	Db 121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAAGACACCCAGTAGCACACTTACC 180 Qy 181 CATGCTGAGAATCCTGGACCTACACTACAGGACCAAGCTGATCATGCCAGCCCAAC 240 Db 181 CATGCTGAGAATCCTGATACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 240 Out of the catgct of the cat	241 CCCTGTGAACAGGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAAGTGCAAAAATACGTGCAAGAAAAGTGCAAGAAAAAGTGCAAAAAAGTGCAAAAAAAGTGCAAAAAAAA	DD 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCTGT 360 Qy 361 GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACTACGGTGTGTGT	OY 421 CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 480	OY 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC 540	541 CAGTICAAGGGAAAITCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC 	OY 601 TCTTACCGAGGAAATGAATAGGACAGTCAACCAGCATGTGCTTTACTGGAACTCC 660 Db 601 TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCTTTACTGGAACTCC 660	Qy 661 CACCTCCTGTGCAGGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 720 	Oy 721 GGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA 780	Oy 781 GTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC 840	QY 841 GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAAGCTTCCGGGGTTTGACTCC 900 b 841 GTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTTCGGGGTTTGACTCC 900 QY 901 TGTGGAAAAGACTGAGAAGAGCAAGATCAAGAGAATCTATGGAGGTTTAAGAGC 960

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RESULT 4
US-10-391-215-2
Sequence 2, Application US/10391215
Sequence 2, Application World 10000543A1
Sepulation No. US20040009543A1
GENERAL INFORMATION:
APPLICANT: KICHEL, STEPAN
APPLICANT: WIEDERWANN, CHRISTIAN JOSEF
APPLICANT: WEIMER, THOMAS
APPLICANT: ROBMISCH, JUERGEN
APPLICANT: FUGNESCH, ANNETTE
APPLICANT: FUGNESCH, ANNETTE
APPLICANT: DOERSAM, VOLKER
APPLICANT: TITLE OF INVENTION: (FSAP) AS RISK FACTOR VII ACTIVATING PROTEAGE
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
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                                                      GCCCACTGCACCGACATAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG
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                                             TYPE: DNA
CRGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No.
US-09-880-107-1668
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Best Local Similarity 100.0%;
Matches 1683; Conservative 0
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1668
LENGTH: 3008
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FILE REFERENCE: 06478.1457-01 CURRENT APPLICATION NUMBER: 08/10/391,215 CURRENT FILING DATE: 2003-03-19 FRIOR APPLICATION NUMBER: 09/912,559 FRIOR FILING DATE: 2001-07-26 FRIOR APPLICATION NUMBER: 0E 100 36 641.4 FRIOR APPLICATION NUMBER: DE 100 50 040.4 FRIOR FILING DATE: 2000-10-10 FRIOR APPLICATION NUMBER: DE 100 52 319.6 FRIOR APPLICATION NUMBER: DE 100 52 319.6 FRIOR APPLICATION NUMBER: DE 101 18 706.8 FRIOR APPLICATION NUMBER: DE 101 18 706.8 FRIOR APPLICATION NUMBER: DE 101 18 706.8 FRIOR FILING DATE: 2001-04-12 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.1 LENGTH: 1683 TYPE: DNA ORGANISM: Homo sapiens	-10-391-215-2 Query Match 99.9%; Score 1681.4; DB 16; Length 1683; Best Local Similarity 99.9%; Pred. No. 0; Matches 1682; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 1 AIGTINGCCAGGANGICTGANGICTGCTGTATAGCTGTGAAAGACA 60	ATGITTGCCAGGATGTCTGATCTCCATGTTCTGTTAATGGCTCTGGTGGGAAAGACA 60	CASTATGATTACAGCTACGAGGATTATAATCAGGAGAGAGAGA	241 CCCISIGNACACGGGGAACTGCCTCGTCCATGGGAACACCTTCACATGCACTGCCTG 500 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAATACGTGCAAAATACGTGCAAGGACACCCATGT 360 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAATACGTGCAAAATACGTGCAAGGACATGT 360 361 GGCCGGGGGCCAATGTCTCATTACCCAGAGTCCTCCTACTACCGCTGTTGTACTGTAAAAC 420 361 GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCTACTACCGCTGTGTCTGTAAAAC 420 361 GGCCGGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACA 420			661 CACCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 720

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 GENERAL INFORMATION:
APPLICANT: KIECHL, STEFAN
APPLICANT: WILDERWANN, CHRISTIAN JOSEF
APPLICANT: WILDERWANN, CHRISTIAN JOSEF
APPLICANT: ROEMISCH, JUERGEN
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1200 1080 1140 1260 1020 1320 1380 960 006 900 960 840 GITACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC 840 540 540 600 600 999 660 720 720 780 420 420 480 480 360 360 GITGCCTACCCAGAGGAAAAGCCCCACCAAACCAAGCTTCCGGGGGTTTGACTCC 841 GIIGCCIACCAGAGGGAAAGCCCCACTGAGCCATCAACCAAGCIICCGGGGTIIGACICC 901 TGTCGAAAAGACTGAGATAGCAGAGAGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC 1081 GCCCACTGCACCATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG AAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGGAGAAGATATTCAAGTACAGCCAC 1141 AAGAAAGAAGATITCAIGAGCAGAGCITIAGGGIGCAGAAGATAITCAAGIACAGCAC TACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAAGCCAGTG 1201 TACAATGAAAGAAGATGAGATTCCCCACAATGATATTGCTTCAAGTTAAAGCCAGTG GATGGTCACTGTGCACAATCCAAATACGTGAAGACTGTGTGCCTTGCCTGAATGGGTCC 1021 ATGCCCCAGGGCCACTTCTGTGGTGGTGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCT CACCTCCTCGTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT GGGGAACACAATTTCTGCAGAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTAAAA rchracceaegeaaaargaaragdacagrcaaccagcargcgreccrrracregaacrec GITACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCAC GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAACAC CCTTACACAGGTCCCAGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC ATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC CAGITICAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTAC TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGGGGAAGGACAAGGACCATGT

RESULT 9
US-10-425-000-17
Sequence 17, Application US/10425000
Publication No. US20040052777A1
Sequence 17, Application US/10425000
Publication No. US20040052777A1
GENERAL INFORMATION:
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Slanche, Francis
TITLE OF INVENTION: Anglogenesis
TITLE OF INVENTION: Anglogenesis
TITLE OF INVENTION: Anglogenesis
CURRENT APPLICATION NUMBER: US/10/425,000
CURRENT APPLICATION NUMBER: US/10/33,675
PRICA FILING DATE: 2002-09-04
NUMBER: OF SEQ ID NOS: 105
SEQ ID NO 17
LENGATION: Artificial Sequence
SEQ ID NO 17
LENGATION: Artificial Sequence
FEATURE:
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CHER INFORMATION: binding protein
US-10-425-000-17 Sequence 11164, Application US/09864761
Facent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, DAVID K.
APPLICANT: HORSEN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILLE REPRESTOR ANALYSIS BY MICROARRAY FILLE OF INVENTION NUMBER: US/09/864,761
CURRENT APPLICANTON NUMBER: US/09/864,761 633 693 61 CAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTTGCAGGAGAATTACAACATGTTT 120 753 813 359 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGACAACCATGT 418 9 694 ATGGAGGATGCTGAAACCCCATGGGATTGGGGAACACACAATTTCTGCAGAAACCCAGATGCG 634 CAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTTTGCAGGAGAATTACAACATGTTT GACGAAAAGCCCTGGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAAATACTGT 574 GATGAÇTGCTATGTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAAC .. 0 Query Match
Best Local Similarity 99.6%; Pred. No. 2.3e-76;
Matches 263; Conservative 0; Mismatches 1; Indels 0;

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REPERBACE: 689200-76

CURRENT APPLICATION NUMBER: US/60/233,617

PRIOR PLING DATE: 2001-09-18

PRIOR PLING DATE: 2000-09-20

PRIOR PLING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR PLING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/235,638

PRIOR PLING DATE: 2000-09-26

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PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27 Query Match Best Local Similarity 49.8 Matches 607; Conservative TYPE: DNA
CORGANISM: Homo sapiens
US-09-954-456-552 469 529 805 Dp ઠે g à g ò OTHER INFORMATION: MAP TO ACCO6097.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN BEAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.0

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.9 PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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PRIOR PELLOATION NUMBER: US 09/774,203
PRIOR PELLOATION NUMBER: US 09/774,203
PRIOR PELLOATION NUMBER: US 09/774,203 TYPE: DNA ORGANISM: Homo sapiens US-09-864-761-11164

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Length 2036;
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Score 117.6; DB 9;
Pred. No. 1.5e-27;
0; Mismatches 559;
       7.0%;
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RESULT 11 US-09-954 456-552 Sequence 552, Application US/09954456 Parent No. US20020115057A1

CCAAG 448

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324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC

7.1%; Score 120.2; DB 9; Length 451; 97.6%; Pred. No. 8.6e-29; arive 0; Mismatches 3; Indels 0

Query Match Best Local Similarity 97.6 Matches 122; Conservative

Gaps ö

1407 1680 1265 1324 TGGGTGGTGTCGGCCGCCCACTGCTTCTCCCACAGCCCCCCCAGGGACAGGGTCTCCGTG 1383 GTGCTAGGGGACCAGGACCTGAAGAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGGAG 1179 AAGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCACAATGATATTGCA 1239 1444 AAGTACATCCCGTACACCCTGTACTCGGTGTTCAACCCCAGCGACCAC---GACCTCGTC 1500 1501 CTGATCCGGCTGAAGAAGAGGGGACCGCTGTGCCACACGCTCGCAGTTCGTGCAGCC 1560 1561 ATCTGCCTGCCCGACCCGGCAGCTTCCCCGCAGGACACAAGTGCCAATTGCGGGC 1620 GGAGGCCCCCTGTGAGAAGGACGGCACCTACTACTACTATGGGATAGTGAGCTGG 1587 GGTGACGGCTGCGGGCTCCACAAGCCGGGGGTCTACACCCGCGTGGCCAACTATGTG 1917 GTGCTGGGCCAGCACTTCTTCAACCGCACGACGACGTGACGCAGACCTTCGAG 1006 CCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGCGCTGATCCACCCTGC --ecriscicacianicia en respensado en esta en e TGGGTGCTCACTGCCCACTGCACCGACATAAAAACCAGACATCTAA-----AGGTG TIGCTCAAGTTAAAGCCAGTGGATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACT GTGTGCTTGCCTGAT-----GGGTCCTTTCCCTCTGGGAGTGAGTGCCACATCTCTGGC 1354 TGGGG-----TGTTACAGAAACAGGAAAAGGGTCCCGGCCAGCTCCTGGATGCCAAAGTC resescentrasaries a se a consecuenta en consecuencia de consecuencia en consecu AGTATGATCTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT 1798 GGGGGGCCCCTGCGAGAAGAACGGCGTGGCTTACCTCTACGGCATCATCAGCTGG GGCCTGGAGTGTGGG-----AAGAGGCCAGGGGTCTACACCCAAGTTACCAAATTCCTG 1213 CIGCGGCCACGIAICAICGGCGGCTCCICCICGCIGCCCGGCICGCACCCCIG---1918 GÁCTGGÁTCÁÁCGACCGGÁT 1937 1180 1240 1300 1681 1528 1266 1120 1384 1621 1588 1858 8 6 8 6 8 6 8 g B & B & B & B & B 8 6 8 à g δ d

18-08-714-708-T. INDO

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                                                                                                      Gaps
                                                                                                                                   AACCCCTGCCAGAATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGT
                                                                                                      54;
) ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D14012
US-09-880-107-1612
                                                                           Length 2036;
                                                                                                      Indels
                                                                        Query Match
7.0%; Score 117.6; DB 9;
Best Local Similarity 49.8%; Pred. No. 1.5e-27;
Matches 607; Conservative 0; Mismatches 559;
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0
LENGTH: 117

TYPE: DNA

ORGANISM: Homo sapiens

PEATURE:

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: OTHER S83182.1, EVALUE 8.00e-60

OTHER INFORMATION: STARSPENDIN HIT: TERREGEL, EVALUE 1.00e-03

OTHER INFORMATION: EST_HUMAN HIT: TERREGEL, EVALUE 1.00e-03

US-09-864-761-27791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117
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Sequence 5509, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MOTITIE, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SSETURNE: 1307
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49.7%; Pred. No. 1.6e-19;
live 0; Mismatches 523;
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100.0%; Pred. No. 4.5e-28;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 117; Conservative
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Best Local Similarity 49.7
Matches 586; Conservative
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; ORGANISM: Mus musculus
US-10-087-192-590
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US-10-087-192-590
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APPLICANT: PRAN. JABATCH G.
APPLICANT: RAN. JABATCH G.
APPLICANT: RAN. JABATCH G.
APPLICANT: CHAN. WARRANG GENOME-DENTED SINGLE EXON NUCLEIC ACID PROBES USFUL, FOR TITLE OF INVENTION: HARMA GENOME-DENTED SINGLE EXON NUCLEIC ACID GENOME TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY CITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY CHAN. MARREN: 19/69/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR PELLICATION NUMBER: 19/69/864,761

PRIOR PELLICATION NUMBER: 19/69/864,761

PRIOR PELLICATION NUMBER: 19/69/823,466

PRIOR PELLICATION NUMBER: 19/69/823,466

PRIOR PELLICATION NUMBER: 19/69/823,466

PRIOR PELLICATION NUMBER: 19/60/823,466

PRIOR PELLICATION NUMBER: 19/60/823,466

PRIOR PELLICATION NUMBER: 19/70/801/0066

PRIOR APPLICATION                                                                                                                                                                                                                                                GGAGGCCCCCTGACCTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGG 1587
                                                                                                                                                                                                                                                                                                                                                                   GGCCTGGAGTGTGGG-----AAGAGGCCAAGTCTACACCCAAGTTACCAATTCCTG 1641
                                                                                                                                                                                                                                                                                                                                                                                                                        1858 GGTGACGGCTGCGGCGCTCCACAAGCCGGGGTCTACACCGGCGTGGCCAACTATGTG 1917
                                                                     1681 cccchégicoccadecacaagideageacectaagaienacaceceacaneaecece 1740
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               AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACTGCCAGGGTGACTCT
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Patent No. US20020048763A1
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EXPRESSIC

UROKINASE PLASMINOGEN ACTIVATOR

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Sequence 10, Application US/10665216
Publication No. US20040043957A1
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Freier

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Pred. No. 2.3e-19;
0; Mismatches 523;
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF URG
TITLE REPENCE: RTS-0188
CURRENT APPLICATION NUMBER: US/10/665,216
CURRENT FILING DATE: 2003-09-19
RICA APPLICATION NUMBER: US/09/821,972
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 2299
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586; Conservative (
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, LOCATION: (59)
US-10-665-216-10
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1297 ACTGTGTGCTTGCCTGATGGGTCCTT----TCCCTCTGGGAGTGAGTGCCACATCTCT 1350
            953 ACCATCTGCCTGCCCCAAGGTTTACTGATGCTCCGTTTGGTTCAGATCACT 1012
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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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SUMMARIES

Description	3955	7603 D	3954	7602	2 hyalur	50	Human m	1412 Homo	3915 Mus	=	Human	Ношо ва	Sequenc	Mus mu	Rattus	Rattu	Mus	Wus.	Σ	A encodi	I15469 Sequence 14	H	Seguenc	Sequenc	mo sap	u	L03546 Bos taurus	X02724 Porcine mRN	X65651 R.norvegicu	X63434 R.norvegicu	X02389 Mouse mRNA	E07615 DNA encodin	~	308 Sequence 3	987	242		36 Desmodus r	<u>ح</u> ۵	51565 Rattu	3697 Rat tissu	989 Des	246 Artificia	184 Sequence	J05082 Vampire bat
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ALIGNMENTS

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AX383955 1 from Patent BP1182258. AX383955	Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryotes, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	1 Boemisch, J., Stoehr, H.A., Feussner, A., Lang, W., Weimer, T., Becker, M., Nerlich, C. and Muth-Naumann, G. Mutants of the factor vii activating protease and methods for their
RESULT 1 AX383955 LOCUS DEFINITION ACCESSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE

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                                      TCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC
                                                                                  CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT
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PR 26-JUL-2000 DE 1003641:4,10-OCT-2000 DE 1055040:4 F 21-OCT-2000 DE 1052319:6,12-APR-2001 DE 1018706:8 PI JUERGEN ROEMISCH, HANS ARNOLD STOEHR, ANNETTE FEUSSNER, WIEGAND
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Detection method with the use of factor VII activating
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/organism='Homo sapiens (human)'.
Location/Qualifiers
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Detection method with the use of factor VII mutant and specific antibody
Patent: JP 2002291486-A 2 08-OCT-2002;
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by mRNA linear PRI 11-FEB-1997
hyaluronan-binding protein=hepatocyte growth factor activator
homolog [human, plasma, mRNA, 2408 nt].
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Choi-Mura, M.H., Tobe, T., Sumiya, J., Nakano, Y., Sano, Y., Mazda, T. and Tomita, M.

purification and characterization of a novel hyaluronan-binding protein (PHBP) from human plasma: it has three EGF, a kringle and serine protease domain, similar to hepatocyte growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenBank staff at the National Library of Medicine created this entry [NGE] gibbsq 179530] from the original journal article. This sequence comes from Fig. 3B.

Location/Qualifiers
      ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC
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/db_xref="taxon:9606" /note="EMBL/GenBank Accession No. D49742" ORIGIN	Query Match 99.8%; Score 1679.8; DB 6; Length 3008; Best Local Similarity 99.3%; Pred. No. 0; Matches 1681; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	OY 1 AIGITIGCCAGGAIGICTGATCTCCAIGITCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60 DD 97 AIGITIGCCAGGAIGICTGATCTCCAIGITCTGCTGTAATGGCTCTGGTGGGAAAGACA 156	Oy 61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCGGACTGGACCCCTGAC 120	Oy 121 CAGTATGATTACAGGTACGAGGATTATAATCAGGAAGAGAACACCCAGTAGCACACTTACC 180	Oy 181 CATGCTGAGAATCCTGACTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 240	Oy 241 CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCTG 300	Qy 301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 360	Oy 361 GGCGGGGCDAATGTCTCATTACCCAGAGTCCTCCTACTACCGCTGTCTCTGTAAACAC 420	Oy 421 CCTTACACAGGTCCCAGGTGCTCCCAGAGGGTTCCTGTATGCAGGCCAAACCCTGCCAG 480	Oy 481 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGAC 540	Qy 541 CAGITCAAGGGAAAITCIGIGAAAIAGGIICIGAIGACGCTAIGITGGCGAIGGCTAC 600	Oy 601 TCTTACCGAGGAAAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 660	QY 661 CACCTCCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 720 Db 757 CACCTCCTTTGCAGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 816 QY 721 GGGGAACACAATTTCTGCAGAAACCCAGAAAGCCCTGGTGGTGTTTATTAAA 780 Db 817 GGGGAACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGGTTTATTAAA 876 QY 781 GTTACCAATGACAAGTGAAATGGGAATACTGTGATGTCTCAGCCTGGCCCAGGAC 840 Db 877 GTTACCAATGACAAAATGGGAATACTGTGATGTCTCAGCCTGAGCCCAGGAC 936 QY 781 GTTACCAATGACAAAATGGGAATACTGTGATGTCTCAGCCTGAGCCCAGGAC 936 QY 781 GTTACCAATGACAAAATGGGAATACTGTGATGTCTCAGCCTGAGCCCAGGAC 936 QY 841 GTTACCAATGACAAAATGGGAAAACCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACCTCC 936 QY 901 TGTGGAAAGACTGAGGAAAAGCCCCACTGAGCATCAACCAAGCTTCCGGGGTTTTAAGAGC 936 QY 901 TGTGGAAAGACTGAGAGAGAGACCCACTGAGCATCAACCAAACAACTTTAAGAGC 1056 QY 901 TGTGGAAAGACTGAGAGAGAGAGACTCAACAAAAGCCCTTAAGGAGCTTTAAGAGC 106 QY 901 TGTGGAAAGACTGAGAGAGAGAGACTCAACAACAACAACAACAACAACAACAACAAAAAAAA
QY 961 ACGGCGGCAAGCACCCATGGCGGCGTCCTCCAGTCCTCGCTTCTGACCATCTC 1020 Db 1057 ACGGCGGCAAGCAACACAAGGAAGGAAGGAAGGAAGGAA	OX 1021 ATGCCCCAGGGCCACTTCTGTGGTGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCT 1080 Db 1117 ATGCCCCAGGGCCACTTCTGTGGTGGGGCGCTGATCCACCCCTGCTGGGTGCTACTGCT 1176	QY 1081 GCCCACTGCACCGACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG 1140	Qy 1141 AAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCAC 1200 	Qy 1201 TACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG 1260 Db 1297 TACAATGAAAGAGATGAGATTCCCCACAATGATTGCATTGCTTCAAGTTAAAGCCAGTG 1356	Qy 1261 GATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGTG	QY 1321 TITCCTCTGGGAGTGACTGCCACATCTCTGGCTGGGGTGTTACAGAAACAGGAAAAGGG 1380	Oy 1381 TCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCGC 1440 1477 TCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCGC 1536	Qy 1441 CAACTCTATGACCACATGATTGATGACGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500	Oy 1501 GGGCAAGACCTGCCAAGGTGACTCTGGAGGCCCCTGACCTGTGAAGAAGACGGCACC 1560 Db 1597 GGGCAAGACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGAACGACCCC 1656	OY 1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAGAAAAGAGGCCAGGGGTCTAC 1620	Qy 1621 ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC 1680 Db 1717 ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGAAGTTG 1776	Cy 1681 TAA 1683 	SULT 6 409021 CUS FINTION SEQUENCE CESION AX409021 RASION AX409021 RASION AX409021 UNCE HOMO SADI UNCE HOMO SADI FERENCE HOMO SADI FERENCE AUTHORS AUTHORS ALVARES, CAUTHORS AUTHORS SOURCE

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	Db 1357 GAIGGTCACTGTGAATCCAAATGGTGAAGATGTTGCTTGCTTG	Db	QY 1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCTGACCTGTGAGAAGGACGGCACC 1560 Db	GGCTT FGGCTT	Oy 1681 TAA 1683 Db 1777 TAA 1779	HUMHGFAL LDOCKS HUMHGFAL

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BC031412
Homo sapiens hyaluronan binding protein MGC:34485 IMAGE:5187066), complete cds.
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                                                    817 GGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA
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I (bases 1 to 2251)

E traubberg, R.L., Feligold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Magner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Gordan, H., Moore, T., Mark, S.I., Mang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carnindi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Garcia, A.M., Gay, L.J., Hulyk, S.N.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.N.,
Villalon, D.K., Muzny, D.M., Godergran, E.J., Lu, X., Gibbs, R.A.,
Sancherz, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

NELL Proc. Natl. Acad. Sci. U.S., 39 (26), 16899-16903 (2002) PRI 07-0CT-2003 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 50 Row: g Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20302151.
Location/Qualifiers NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capabs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A. Ή. Direct Submission Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (WGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, 2, mRNA (cDNA clone l. .2251 /gene≃"HABP2" gene

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       TCTTACCGAGGGAAAATGGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC
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                                                                                                     GGGGAACACAATTTCTGCAGAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA
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                                          CACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGA
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S Isogai, T. and Yamamotoo, J.
L Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-1018, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO CDNA sequencing project supported by Ministry of Economy,
Trade and Industry of Japan; CDNA full insert sequencing: Research
Association for Biotechnology (RAB); CDNA ilbrary construction:
Helix Research Institute (HRI) (supported by Japan Key Technology
Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and
Biotechnology Center, National Institute of Technology and
Evaluation; clone selection in for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, B., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
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Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Salto, K.,
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Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K.,
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Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
Unpublished
                                                         ANLICEVIES
Mus musculus cDNA fis, clone TRACH2024735, moderately similar to AKI28915
AKI28915
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oligo capping; fis (full insert sequence).
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Best Local Similarity 80.3%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 325;
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AUTHORS
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/db_xref="Myatalroni
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22122612.
Location/Qualifiers
1. 2119
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/ strain="FYB.N"
/ strain="FYB.N"
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/clone="MGC:28705 IMAGE:4245577"
/tissue_type="Kidney, normal. 5 month old male mouse."
/lab_host="NGI GGAP_Kid14"
/lab_host="DH10B"
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|db_xref="CDD:smart00020"
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DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center code: BCM-MGSC Center rode: BCM-MGSC Contact: amg@bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
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/note="KR; Region: Kringle domain"
/boxref="CDD:smart00130"
866. .1579
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AL Submission

AL Submitted (29-MG-2001) Sanger Centre, Hinxton, Cambridgeshire, Direct Submission

AL Submitted (29-MG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, WK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

On Aug 31, 2001 this sequence version replaced gi:14596344.

On Aug 31, 2001 this sequence version replaced gi:14596344.

On Aug 31, 2001 this sequence version replaced gi:14596344.

On Ly a sequence assembly data is compared from overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequence with a core of the overlapping clone, as we submit sequence was finished as follows unless otherwise noted all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequenced with an alternate one plasmid subclone or more than one Mi3 subclone; and the associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw: SMRSPROT; T:, TREMBL; Wp:, WoRNDEP; Information on the WoRNDEP database can be found at http://www.sanger.ac.uk/Projects/Celapans/wormpep This sequence was generated from part of bacterial clone contrigs of human chromosome 10, constructed by the Sanger centre Chromosome 10 http://www.sanger.ac.uk/Projects/Celapans/wormpep This sequence of Phere and Dong. For futther information can be found at http://www.sanger.ac.uk/Projects/Celapans/wormpep This sequence of perer de Jong. For futther details see http://www.chori.org/bacpac/home.htm

VECTOR: PBACe3:6

Location/Qualifiers

Substance of clone RPI1-48HH12 is at 111825 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL390197 188349 bp DNA linear PRI 29-AUG-2001
Human DNA sequence from clone RP11-190F19 on chromosome 10,
complete sequence.
AL390197
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188349)
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/clone="RP11-190F19"
/clone="RP12-12187"
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(AL133482). Assembly confirmed by restriction digest."
                                                                1470 CCTGTGAGAAGGATGGAACTTACTACGTCTACGGGATTGTAAGCTGGGGCCAGGAATGTG
                                                                                                                                    1601 AGAAGAGGCCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCA
                                                                                                                                                                                             1541 CCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTG
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AUTHORS
TITLE
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Sequencing of Human Chromosome 10
Unpublished
Unpublished
Unpublished
Smith, D.R.
Smith, D.R.
Direct Submission
Direct Submission
AL Submitted (04-1988) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA
Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing
Technology. Data may contain low quality seq uence and BAC/Cosmid
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the accession number will be preserved.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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// Mol_type="genomic DNA"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Score 261.2; DB 9;
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammālia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                  AGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGCACGGGGGGCAAGCACCCATGGCAG
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                                                                                                                                             ACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAG
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Patent: W0 0188188-A 123 22-NOV-2001;
School Juridical Person Nihon University (JP)
Location/Qualifiers
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Best Local Similarity 84.4%; Pred. No. 8.7e-61;
Matches 271; Conservative 0; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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Sequence 123 from Patent WO0188188.
AX305372.
AX305372.1 GI:17644923
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GAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGACGTTGCCTACCCAGAGGAAAGCCCC

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0; Mismatches

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AC115771 204214 bp DNA linear HTG 18-JUN-2003
Mus musculus clone RP23-116D4, WORKING DRAFT SEQUENCE, 11 ordered
                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 204214)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-116D4
                                                                                                            HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
                                                                                           GI:31880182
                                                                                                                                                                                                                                                                                     (bases 1 to 204214)
                                                                                                                                                                                                                                                               Jnpublished
                                                                         AC115771
AC115771.
                                                       pieces
                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                      LOCUS
DEFINITION
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AUTHORS
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Birrenses 1 to 204241.

S. (Undersol 1. C. 204241.

S. Anderson, S. Barra, N. Bastlein, V. Bloom, T. Soggalavdky, J., Changy, A. Anderson, S. Barra, N. Bastlein, V. Bloom, T. Soggalavdky, J., Colangoplano, A. Colango, J. Camarate, J., Camarate, J., Camapplano, A. Collymore, A., Cooke, A., Cooke, P., DeArellano, K., Campoplano, A., Collymore, A., Cooke, M., Cooke, M. Colango, J. Callymore, A., Cooke, M., Cooke, M., Colango, J. Callymore, C. Cook, M., Cooke, M., C

TITLE JOURNAL AUTHORS REFERENCE

TITLE JOURNAL

COMMENT

------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seg.wi.mit.edu

/note="assembly_fragment'

misc_feature

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**NOTE: This is a 'working draft' sequence. It current consists of II contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced to 10062 by in length 100763 70763 70762 contig of 671 by in length 11533; gap of 100 by 11534 72371; contig of 671 by in length 11534 72371; contig of 1449 by in length 11534 72471; gap of 100 by 11534 72471; gap of 100 by 11534 72471; gap of 100 by 11534 72471; gap of 100 by 11534 72471; gap of 100 by 11534 72471; gap of 100 by 11534 72471; gap of 100 by 11534 72472 73920; contig of 1038 by in length 115466 86603; contig of 1038 by in length 11555 gap of 100 by 11553 by in length 11553 gap of 100 by 11553 by in length 11553 by in length 11553 by 11553 by 115555 contig of 15553 by in length 115555 contig of 15553 by in length 115555
                                                                     Center clone name: 15.04

Center clone name: 116.04

Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 202492 bases at least Q20

Consensus quality: 202492 bases at least Q20

Consensus quality: 202921 bases at least Q20

Insert size: 210000; agarose-fp

Insert size: 23314; aum-of-contigs

Quality coverage: 12.4 in Q20 bases; sum-of-contigs
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L23373
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of 14305 bp in length
100 bp
of 18201 bp in length
100 bp
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. 70562
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71534. .72371
/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:10090"
/clone="RP23-116D4"
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70763. .71433
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(bases 1 to 224208)
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Barder, M., Baca, B., Baden, H.,
Banyalechi, V., Bandaranaike, D., Barber, M., Baca, B., Baden, H.,
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Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Centr, A.,
Clacko, J., Chavez, D., Chen, G., Copie, M., Cree, A., D. Souza, L.
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.
Delgado, O., Denson, S., Deramo, C., Tong, Y., Dinh, H., Divya, K.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Egan, A., Escotto, M., Eugene, C., Evers, P., Fraser, C., Coy, Espan, A., Escotto, M., Eugene, C., Evers, P., Fraser, C., M., Gane, S., Dunn, A., Dural, B., Baves, K.,
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
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Karpathy, S., Kelly, S., Kelly, S., Khuly, S., Khang, L., Kovar, C.,
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Rattus norvegicus clone CH230-131J10, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          958 AGCACGGCGGCCAAGCACCCAIGGCAGGCGICCTCCAGICCTCGCTGCTTCTGACCAIC 1017
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                              Length 204214;
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AC106236.5
HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
Rattus norvegicus
Rattus norvegicus
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136063. .181391
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181492. .204214
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Matches 201; Conservative
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AUTHORS
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KEYWORDS
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on May 13, 2003 this sequence version replaced gi:24942489.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rarl/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table. manujum, D., matchin, A., matchin, A., matchine, B., Mandray, S., McLeod, M.P., Mill, T.Z., Menen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Morris, C., Mall, D., Navton, N., Murphy, M., Nair, L., Nankervis, C., Nail, D., Newton, N., Nguyen, M., Norris, S., Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Panerarak, S., Paul, H., Perez, A., Perez, L., Pfannkon, C., Plopper, F., Poindexter, A., Perez, A., Perez, E., Pu, L.-L., Puazo, M., Reily, M., Ren, Y., Regier, M.A., Reigh, R., Reilly, M., Ren, Y., Redter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Rais, S., Shen, H., Shetty, J., Shavatsbeyn, A., Stock, G., Shatsman, S., Shen, H., Shetty, J., Shavatsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sheed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sheed, A., Sosa, J., Sheed, A., Sodergren, E., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Stang, J., Waldran, D., Waldron, L., Walker, B., Wang, J., Walght, D., Waldren, R., Walder, S., Yen, J., Yoon, J., Walght, D., Wright, R., Walse, R., Walder, B., Walder, B., Waldrin, D., Waldren, A., Smith, H.O., Waistner, A., Weiss, R., Moden, H., Wolte, F., Waistner, A., Weiss, R., Smith, D., Von, L., Yoon, J., Yakub, S., Yen, J., Yoon, J., Yakub, S., Thao, S., Dunn, D., Von, Waistner, Submission

M. Direct Submission

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M. Direct Submission NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is Worley, K.C.
Direct Submission

Submission

Submission

Eaylor Plaza, Houston, TX 77030, USA

Tobses I to 224208)

Rat Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.

Direct Submission Web site: bcw.

Web site: bcw.

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: pcoject Information

Conter project name: GRCQ

Center clone name: GRCQ

Center clone name: GRCQ

Conter project name: GRCQ

Consensus quality: 213390 bases at least Q40

Consensus quality: 216800 bases at least Q30

Consensus quality: 216809 bases at least Q30

Consensus quality: 216809 bases at least Q30

Consensus quality: 216899 bases at least Q30

Consensus quality: 216899 bases at least Q30

Consensus quality: 216999 bases at least Q30

Consensus quality: 216999 bases at least Q30

Consensus quality: 216999 bases at least Q30

Consensus quality: 216299 bases; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. Center: Baylor College of Medicine Center code: BCM

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10868 TCCATGCCCCAAGGCCACTTCTGTGGGTTCCCTGATTCACCCTTGCTGGGTGCTCACT 70809
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9.6%; Score 161; DB 2; Length 224208;
Best Local Similarity 76.7%; Pred. No. 2.8e-36;
Matches 197; Conservative 0; Mismatches 60; Indels 0; Gaps
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Human

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Length 3008;

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                                                                                                                                                                                                                                                                                                                                                                                                                              Gene, liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                              GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCCTGACCTGTGAGAAGGACGGCACC
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The present invention describes nucleic acid sequences (I) having a different degree of expression in hepatoblastoma from their expression in cormal liver tissue. ACCS1116 to ACCS1121 represents specifically claimed examples of (I). Also described: (I) nucleic acids stringently compared in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;
expressed sequence tag; EST; probe; chemotactic; proliferative;
immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
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proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft ve host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, astham, allergies, applastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
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thrombolytic, antilnflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiuleer; osteopathic; neuroprotective; nootropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; wyeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss. 99WO-US024206. 98US-0104436P (GEMY) GENETICS INST INC WO200021991-A1. 15-OCT-1999; Homo sapiens 15-0CT-1998; 20-APR-2000.

Evans Mccoy JM, Lavallie ER, Collins-Racie LA, Treacy M, Bowman MR; Jacobs K, Merberg D,

ς;

WPI; 2000-317938/27.

Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTS), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders.

Claim 1; Page 549; 803pp; English.

AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTS), isolated from human, mouse, chicken and rat tissue cources. The sBSTS can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; hiromobylytic; antiinflammatory; cytostatic; antibacterial; antidiabetic; antibacterial; antidiabetic; antibacterial; antidiabetic; antibacterial; antidiabetic; antibacterial; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be identification and isolation of full-length on the sESTs are useful as probes for the identification and isolation of full-length on the sESTs can be identification and isolation of full-length on the sESTs can be considered by the sESTs. Proteins encoded by the sESTs are useful as says for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (asthma), mysolador lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (castma), mysolado cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (chaemophila, thrombosis), inflammatory disorders (crohi, sumours, bacterial, fungal or viral infections, depression and disorders (haemophila, thrombosis), inflammatory disorders (crohi, sumours, bacterial, fungal or viral infections, depression and psoriasis, apa45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention

Sequence 617 BP; 165 A; 169 C; 148 G; 135 T; 0 U; 0 Other;

ò 0; Gaps Query Match 31.3%; Score 526.4; DB 3; Length 617; Best Local Similarity 99.8%; Pred. No. 1.5e-139; Matches 527; Conservative 0; Mismatches 1; Indels 0.

9 1 AIGITIGCCAGGAIGICIGAICICCAIGITICIGCIGITAAIGGCICTGGIGGGAAAGACA 84 AIGITIGCCAGGAIGICIGAICICCAIGIICIGCIGIIAAIGGCICIGGGGAAAGACA 120

CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCCAGTAGCACATTACC 180 121

GCCTGTGGGTTCTCCCCTGATGTCTTTATTGGAAAGCCTGGACCGAGACTGGACCCCTGAC 203

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240 300 383 360 443 420 503 480 563 263 323 444 GGCCGGGGCCAAIGICTCAITACCCAGAGICCTCCCIACTACCGCTGTGTCTGTAACAC CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAAACACCAGTAGCACACTTACC CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT GGCCGGGGGCCAATGTCTCATTACCCAGAGTCCTCCTTACTACCGCTGTGTCTGTAAAACAC CCTTACACAGGTCCCAGGTCCCAAGTGGTTCCTGTATGCAGGCCAAAACCCCTGCCAG CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGGCCAAAC 611 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGT 481 564 181 264 241 324 301 384 361 421 204 g g $\dot{\delta}$ d ઠ g ò g g & Op ઠે ð

ACH21030;

BP.

ACH21030 standard; cDNA; 428

13-OCT-2003

Human adult liver cDNA #642.

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.

17-APR-2003.

30-JUL-2001; 2001US-00918995.

30-JUL-2001; 2001US-00918995

(DRMA/) DRWANAC R T. (LABA/) LABAT I. (STAC/) STACHE-CRAIN B (DICK/) DICKSON M C. (JONE/) JONES L W.

m.

Stache-Crain B, Drmanac RT, Labat I,

ĽW.;

Jones

Dickson MC,

WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA

Claim 1; SEQ ID NO 8242; 44pp; English

The invention relates to an isolated polynucleotide comprising any one of 18043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences

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are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensias, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample condition (as expression profile of a schaemia occlusive incompression profile of a is useful for examining the ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AR199202 to AB199912, encoding the protein sequences in ABS77020 to ABB57374) or by determining the protein sequences in ABS77020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or indicator when screening for ischaemic condition related sequence. PCR primers for a mouse ischaemic domatic neglence, which are used in the exemplification of the present invention
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                                                                                                                              Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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Ishii
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Best Local Similarity 84.4%; Pred. No. 3.5e-58;
Matches 271; Conservative 0; Mismatches 50;
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   Nagata
                                                                                                                                                                                                                                                                                                                     English
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   Takahashi Y,
                                                                                                                                                                                                                                                                                                                     Claim 2; Page 351-352; 2690pp;
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       Asai S,
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       Ishikawa K,
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ABA58323/c
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 CCAGAGICCTCCCTACTACTGCTGTGTAAACACCCTTACACAGGTCCCAGCTGCTC
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97.6%; Pred. No. 1.1
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632566.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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AAK32096 standard; DNA; 451 BP.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GS-00024263.
                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
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Best Local Similarity 97.6
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 6628; 639pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR,
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AAI37947 standard; DNA; 451 BP.
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21-SEP-2000; 2000US-023468TP.
7-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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Best Local Similarity 97.6
Matches 122, Conservative
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exon nucleic acid probes useful for analyzing
                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                          391 ccadadricereceraeracederidrereraabaacaeeerraeaeadareeeadeereere
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                                                                                                                                                                                                                          Gaps
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hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
                                                                                                                                                                                            Length 451;
                     Example 4; SEQ ID NO 6411; 650pp + Sequence Listing; English.
                                                                                                                                                                  Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                             DB 4;
                                                                                                                                                                                            Score 120.2; DB 4
Pred. No. 1.1e-23;
0; Mismatches 3
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gene expression in human adult liver.
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2000US-0207456P.
2000US-00608408.
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; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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ID ABS31791 standard; DNA; 451
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                                                                                                                                                                                            Query Match
Best Local Similarity 97.6
Matches 122, Conservative
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                 CCAGAGICCICCCTACTACCGCTGIGICTGTAAACACCCTIACACAGGICCCAGCTGCTC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                               324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC
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                                                                                                              Example 4; SEQ ID NO 6653; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                             Sequence 451 BP; 116 A; 102 C; 127 G; 106 T; 0 U; 0 Other;
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Pred. No. 1.1e-23;
0; Mismatches 3; Indels
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               DR.
                                                                                    gene expression in human bone marrow.
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21-SEP-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
64-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
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Best Local Similarity 97.6%;
Matches 122; Conservative (
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AAK06420 standard; DNA; 451
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               Chen
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                                            WPI; 2001-488900/53
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                Hanzel
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                  SG,
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                  Penn
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for

WPI; 2002-114183/15.

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liver, comprising one of 13100 defined mucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCCAATGTCTCATTAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                        451 TCCTACAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGGCCAATGTCTCATTAC 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher; disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; saxcoidosis; pulmonary hæmosidærosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary hveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.
    measuring human gene expression in a sample derived from human adult
                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                          7.1%; Score 120.2; DB 4; Length 451;
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hes 3; Indels
                                                                                                                                                                                                                                                                                                                        Local Similarity 97.6%; Pred. No. 1.1e es 122; Conservative 0; Mismatches
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30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from the human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array, identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting a t least one exon from genomic sequences of the array; identifying exons in a least one exon from genomic sequences of the eukaryote; and (b) derecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung man, comprising (a) algorithmically predicting specific hybridisation of detectably labeled nucleic acids from eukaryote lung man, comprising (a) algorithmically defentioal to the probe for a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray, assigning exons to a single exon microarray having a probe with the exon, where a common pattern of the exons should be assigned to a single gene, a peptide comprising on microarray and for the exons in the subset for gene expression and year end for identifying exons in a gene, particularly using human conservable man and for the study of lung diseases such as astima, lung cancer, chronic obstructive pulmonary disease (CODB), intersettial lung derived minha and for the study of lung diseases such as astima, lung cancer, chronic obstructive pulmonary disease (CODB), intersettial lung disease (LID), familial idiopathic pulmonary fibrosis, pulmonary hardones such 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 TCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTAC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 CCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACACCCTTACACAGGTCCCAGCTGCTC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 CCAGAGICCICCTACTACGGCTGTGTGTAAACACCCTTACACAGGTCCCAGGTGCTC
                                            Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                         measure gene expression in human lung samples.
                                                                                                                            Claim 1; SEQ ID NO 6854; 634pp; English.
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 19224; 639pp + Sequence Listing; English
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100.0%; Pred. No. 4.9e-23;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                             26-MAY-2000; 2000US-0207456P.
30-UN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0063266.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GS-00024263.
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Best Local Similarity 100.0
Matches 117; Conservative
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                                                                                              WO200157277-A2.
                                                                Homo sapiens
                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                               09-AUG-2001
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

Human foetal liver single exon nucleic acid probe #19224.

Search completed: May 25, 2004, 06:30:49 Job time : 473 secs

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Gaps . 0 332 TGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTACCCAGAGTC 391

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CB156834 K-EST0215
CB162144 K-EST0212
CB162144 K-EST0222
CB594245 ACENCOURT
BE032018 130809 MA
AA217892 mv54408.r
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AW610902 un13910.y
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ALIGNMENTS
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CB568162018
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BX325239
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AUTHORS
TITLE
JOURNAL
COMMENT
  BX325239 BX325239
BX463023 BX463023
BI761782 603046775
BX431866 BX431866
                                                                               May 25, 2004, 05:42:15 ; Search time 3059 Seconds (without alignments) 16429.568 Million cell updates/sec
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1683
1 atgtttgccaggatgtctga......aaagtgaaagtggcttctaa 1683
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            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Database

No. Result

Minimum Maximum

Db 925 AGTTACCAAGGTGAATGGGGAATAYTGTGATGTCTCAGCCTGAGGA 984 Qy 840 CGTTGCCTACCAGAGGAAAGCCCACTGAGCCATCAACCTCCAGCCTGAGCCCAGGA 984 Db 985 CGTTGCCTACCCAGAGGAAAGCCCACTGAGCATCAACCTTCSGGGGTTTGACTC 899	ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1008) AUTHORS Li,W. B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length CDNA libraries and normalization JOURNAL Contact: Genoscope COMMENT Generact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 \$1006 EVRY cedex - France BP 191 \$1006 EVRY cedex - France Inbrary was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5634.f For more information about this cluster, see	This is the contact of the contact o	ORIGIN Query Match Query Match Best Local Similarity 93.4%; Pred. No. 7.5e-208; Matches 840; Conservative 31; Mismatches 19; Indels 9; Gaps 7; Qy ATGTTTGCCAGGAIGTCTGATCTCCATGTTCTGCTGTTAATGGCTCTGGTGGAAAGACA 60 Db 110 ATGTTTGCCAGGATGTCTCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 169	OY 61 GCCTGTGGGTTCTCCCTGATGTCTTATTGGAAAGCCTGGACCCCAGACCCCTG-A 119
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1 (bases 1 to 891)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: Gapber Gamail.nih.gov

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAMI1467 row: e column: 19
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                                          299 IGGCICCTITCTCTGGGAATAAGTG - - TCAGAAAGTGCAAAATACGTGCAAGGACAACCC
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Enail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Invitrogen. This sequence belongs to sequence cluster 5634.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSOBAGO65ZHOS CSO6184 i&cluster=5634.f.
Contect: Feng Liang Email: filang@lifetech.com URL:
Contect: Feng Liang Email: filang@lifetech.com URL:
Location/Qualifiers
Location/Qualifiers 755 815 120 875 180 935 995 BX431866
BX411866 Homo sapiens FETAL LIVER Homo sapiens cDNA clone CCODMO04YK02 5-PRIME, mRNA sequence. 9 Homo sapiens (human)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001) GGAGGATGCTGAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCAGATGCGGA CGAAAAGCCCTGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGA AACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAGAGAAGATCAA GAGAATCTATGGAGGCTTTAAGAGCACGGGGGAAGCACCCATGGCAGGCGTCCCTCCA gcaccarcaraccarceatrescarrescarrescarrescaracacarrescara TGTCTCAGCCTGCTCAGCCCAAGGACGTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATC tch 38.3%; Score 645.4; DB 13; Length 889; al Similarity 91.2%; Pred. No. 5.9e-173; 696; Conservative 0; Mismatches 66; Indels 1; Gaps 801 GGATTGGGGAAACACCAATTTCTGCAGAAAACCCAGATGCCGACGAAAAAGCCCTGGTGC BX431866.1 GI:30789052 861 rrharraadroacca 877 Query Match Best Local Si Matches 696; 816 876 .954 61 181 936 772 VERSION KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 4 BX431866 LOCUS ACCESSION FEATURES ORIGIN QQ 임 g à à δ 쉽 8 g

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Manmalar Surfactorial Fillmaces, Cacarinana, Manmalar Surfactorial Fillmaces, Cacarinana, Chu, M.Y., Kim, M.R., S. Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001
Unpublished (2002)
Unpublished (2002)
Unpublished (2002)
Unpublished (2002)
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S.Z. Bean-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 07
High quality sequence stop: 576.
Liceation/Qualifiers
                                                                                                                                                        EST 29-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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CB156834.1 GI:28141962
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FEATURES ORIGIN 8 6 g a 8 g ò ò å q ò g 8 엄 ે ద ठे Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 663)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
ZIC Frontier Korean EST Project 2001
Unpublished (2002) EST 30-JAN-2003 974 ACCCATGGCAGGGGTCCTCCAGTCCTCGCTGCCTCTGACCATCTCCATGCCCCAGGGCC 1033 ö laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell 853 157 GCTCCCGGCATAAGCCGAGATCCAAGTTCACCTGTGCCTCTCCCGACCAGTTCAAGGGGA 517 613 673 AAATGAATAGGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTCTTGC 397 733 337 793 TCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAAGTTACCAATGACA 277 276 AGGIGAAAIGGGAAIACIGIGAIGICICAGCCIGCICAGCCCAGGACGIIGCCIACCAG AGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTG 913 914 AGATAGCAGAGAGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGCACGGGGGGAAGC 973 GCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGACCAGTTCAAGGGGA 553 AATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGGCTACTCTTACCGAGGGA 457 97 AGGAGAATTACAACATGTTTATGGAGGAGGATGCTGAAACCCATGGGATTGGGGAACACAATT 216 AGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCCTGTGGAAAGACTG AATTCTGTGAAATAGGTTCTGATGACTGCTATGTTGGCGATGCCTACTCTTACCGAGGGA AAATGAATAGGACAGCATGCGTGCCTTTACTGGAACTCCCACCTCCTTGC AGGAGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATTGGGGAACACATT TCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAAGTTACCAATGACA AGGTGAAATGGGGAATACTGTGATGTCTCAGCCTGAGCCCCAGGACGTTGCCTACCCAG AGATAGCAGAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAAAGCACGGCGGCAAGC Gaps ö 576; Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea K.EST0222650 L17N670205nl Homo sapiens cDNA clone L17N670205nl Homo sapiens cDNA clone L17N670205nl-17-H10 5', mRNA sequence. CB162144
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r EST 03-APR-2003
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musculus cDNA c
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AGENCOURT 12929103 NIH MGC 177 Mus IMAGE: 30310462 5', mRNA sequence.
             Fax: +82-42-860-4409
Email: yongeung@mail.kribb.re.kr
Plate: 17 row: H column: 10
High quality sequence stop: 663.
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EST.
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CBS94245
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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1326

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1195 AGCCACTACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAG 1254 ઠે /orgatisms: musualus."
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D. 62 Contact: ACCET. Straight of the straight of th 715 GGGATTGGGGAACACACAATTTCTGCAGAACCCCAGATGCGGACGAAAAGCCCTGGTGCTTT 3 escarcecacacacacartricicacacaaacceacaasaceacacacaaaceergerere 775 ATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCCTGCTCAGCC 835 CAGGACGITGCCIACCCAGGAAAGCCCCACCAGCCAICAACCAAGCITCCGGGGTTT 123 cereacacectraacecadregaaaceerreregacerereareareaceerecadeerre 303 ACCTCCATGCCCCAAGGCCACTTCTGTGGGGGCGCCCCGATCCACCCTGCTGGGTGCTC 1; Gaps DB 14; Length 736; Query Match 27.0%; Score 454.2; DB 14; Length 7 Best Local Similarity 80.8%; Pred. No. 2.9e-118; Matches 542; Conservative 0; Mismatches 128; Indels /organism="Mus musculus" REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES ORIGIN g 임 à d ò ò ď d à 셤 à ò 임 ò

රු දි	1195	AGCCACTACAAAGAAATGAAATCCCCACAATGATTGCATTGCTTAGGTTAAAA 1233
: è	1255	CCAGTGGATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGAT 1314
QC QC	5.4	CCAGTGGGTGGTCACTGTGCTCTGGAATCCAGATATGTGAAGACTGTATGTTTGCCAGC 602
ò	1315	GGGTCCTTTCCCTCTGGGAGTGAGTGCCACATCTTGGCT-GGGGTGTTACAGAAACAGG 1373
QQ	603	GACCCCTTTCCCTCTGGAACTGAGTGCCACATCTCTGGCTGG
ò	1374	13
අු	663	GGAAGGGTCC 673
RESULT 8 BE032018 LOCUS DEFINITION ACCESSION KEYWORDS	8 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BE012018 592 bp mRNA linear EST 09-JUL-2000 130809 MARC IPIG Sus scrofa cDNA 5', mRNA sequence. BE012018 1 GI:8327027 EST 50508 (big)
ORGANI	Ś	is scrofa Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, mmaisa, Enthera: Cetartiodactvla, Suina, Suidae, Sus.
REFERENCE AUTHORS		<pre>th,T.P.L., Freking,B.A., Cho,J., Rohrer,G.A., Pertea,G., Sultana,</pre>
TITLE		ackenbush, J. and Keele, J.W. orchine gene discovery by normalized cDNA-library sequencing and ST fluster assembly
JOURNAL MEDLINE PIEMER		amm. Genome 13 (8), 475-478 (2002) 2023189
COMMENT	}	Dutact: Smith TPL DAA, ARS, US Meat Animal Research Center D Box 166, Clay Center, NE 68933-0166, USA
	пны	
	A1 S 40 E	ingle pass sequencing. Bases called and alt trimmed with phred 0.980904.e. Vector identified by cross_match with the -minscore 18 of minmatch 12 options.
	սես ըս իս ն	FORWARD: AGGARACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG Plate: 69 FOW: K Column: 12
FEATURES sou	H	ed primer niindelegement. Location/Qualifiers 1592
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ORIGIN		
Quer, Best Match	Query Match Best Local S Matches 518	h Similarity 86.0%; Pred. No. 1.4e-117; 18; Conservative 0; Mismatches 69; Indels 15; Gaps 1;
δ	522	CACCIGIGCCTGTCCCGACCAGCTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGACTG 581
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ζ	582	CTATGTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGC 641

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Site_2: Sall; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library. |"
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8
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                                                                                                                                         DB 12;
                                                                                                                                       ch 26.6%; Score 447.2; DB 12; al Similarity 77.7%; Pred. No. 3.1e-116; 580; Conservative 0; Mismatches 158;
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clone="IMAGE:4975384"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Tobases 1 to 802)

RS NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs.remail.inh.gov

Tissue Precurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LibNL at:

High quality sequence stop: 785.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG972579 802 bp mRNA linear EST 12-JUN-2001 602841165F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:4975384 5., mRNA sequence. BG972579 GI:14360216
                                                                                                                                                                                                                                                                                                                                                                                                                                 1002 GCTGCCTCTGACCATCTCCATGCCCCAGGCCACTTCTGTGGTGGGGGGGCGCTGATCCACCC 1061
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 CTATGTTGGTGACGGCTACTCTTACCGAGGGAAGTGAGTAAAACTGTCAACCAGCACCACC
                                                 GIGCCITIACIGGAACTCCCACICCTCTTGCAGGAGAATTACAACAIGITTATGGAGGA
                                                                       GIGCCTTTACTGGAACTCCCACCTCCTTGCAGGAGAATTACAACAIGTTTATGGAGGA
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                                                                                                               TECTGAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAA
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/db_xref="taxon:10090"
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Mus musculus (house mouse)
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EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Eukaryota; Macaroa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (base; 1 to 751)

Sis NIH-Moch ther; Mac. nci.nih.gov/.

Is National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.inh.gov

Tissue Procurement: Jofffrey E. Green, M.D.

Contact: Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov. oclumn: 08

High quality sequence stop: 747.

High quality sequence stop: 747.
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602912432F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5053663 5',
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/clone="IMAGE:5053663"
/lab_host="DH10B (Ti phage-resistant)"
/lab_host="DH10B (Ti phage-resistant)"
/clone lib="MCI (GAP_Li9"
/note="Organ: liver; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: SAll; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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The WashU-HMM house EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMM mouse EST Project
WashU-HMM mouse EST Project
WashU-HMM mouse EST Project
WashU-HMM mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                          Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                     CCGGGGCCAATGTCTCATTACCCAGAGTCCTCCTACTACCGCTGTGTCTGTAAAACACCC 422
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                                                                                                                                                                                                                                                                                                     TCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGTGG 362
                                                                                                 CTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGACCA 122
                                                                                                                   cccraadaacccccacradracr----argaagacdardarccardccadrcdaccc 235
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                                                 4 TITGCCAGGATGTCTGCATCTTCTGCTGTTAATGGCTCTGGGGAAGAAGACGC-
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                         Gaps
                         10;
 Length 751;
                         Indels
  DB 12;
Score 435.4; DB 12;
Pred. No. 7.2e-113;
0; Mismatches 156;
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25.9%;
78.0%;
 Query Match 25.9
Best Local Similarity 78.0
Matches 589; Conservative
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i370 bp mRNA linear EST 12-MAR-2002 i370:02 mRNA linear EST 12-MAR-2002 i370:03.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5944156 5' similar to TR:014520 014520 BMS08620. GIKE PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (basea I to S70, Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
  RESULT 12
BM508620
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/note="Vector: pSPORT1; Site 1: Not 1; Site 2: Sal I; Five | Incaries representing E10:5/12.5 pancreatic bud, E16.5 | Incaries representing E10:5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult pancreas, and adult islets of Langerhans were seperately constructed using superScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and Size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with single-stranded mixed library plasmid mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Glbbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium

Au Upublished (2000)
Other ESTS: 1i37h03.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Brdocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-8557
Email: deltonobiohp, harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Library was constructed by Dr. Douglas Melton DNA sequencing on obtaining a clone please contact: Juliana Brown
(brown@fas harvard.edu)
MGI:2007028 This sequence now available from the IMAGE consortium,
for chose orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 435.
Location/Qualifiers
Library
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llarity 85.0%; Pred. No. 5.7e-112;
Conservative 0; Mismatches 85; Indels
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Best Local Simi:
Matches 483; (
                                                                                                                                                                                                                                                                                    TITLE
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 665)
Bajao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.

Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 25-JUL-2003
                                                                                                GCCTGTGGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120
                                                                                                                                                                                                                                          164 GACTATTACTACAGCTATGAGCAGTCCAGCCCAGACGAAGACCCCAGTGTCACGCAGACC 223
                                                                                                                                                                                                                                                                                                                                                                                      CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 300
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B0809C08-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0809C08 IMAGE:30468319 5', mRNA sequence.
                                                 44 AIATITIGICAGGAIGIAGGIGITICCGIGICCTGCTGCTAATCGCCCTGGTGGAAGICA 103
                                                                                                                                         104 drcaredederereargarerecricarresececeeagaeeeagarnegaeeeeegar 163
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                                                                                                                                                                                           121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCAGTAGCACATTACC
                                                                                                                                                                                                                                                                                         181 CATGCTGAGAATCCTGACTGGTACTACACTGAGACCAAGCTGATCCATGCCAGCCCAAC
                                                                                                                                                                                                                                                                                                                                  224 ACCCCTGAGAACCCCGACTGGTACT----ATGAAGACGATGATCCATGCCAGTCCAAC
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     ATGITTGCCAGGATGTCTGATCTCCATGTTGCTGTTAATGGCTCTGGTGGGAAAGACA
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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5', mRNA sequence.
BET88188
                                              TOTGGCTGTGGGGAAAACAGGAAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC 1407
                                                                                                                                         AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT 1527
                                                                                                                                                                                                                                                                                                                                  GGAGGCCCCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGG 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                GOCCTGGAGTGTGAGAAGAGGCCAGGGGTCTACACCCAAGTTACCAAATTCCTGAATTGG 1647
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| strain="kyB/N"
| strain="kyB/N"
| strain="kyB/N"
| db_xef="twan=1000"
| clone="INAE.4241642"
| lab_host="DH10B (T1 phage-resistant)"
| clone lib="NCI CGAP Kid14"
| note="Coran: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
| site_2: Sali; cloned unidirectionally. Primer: Oligo dT.
| Average insert size 1.75 kb. Constructed by Life
| Technologies: Note: this is a NCI_CGAP Library. | "
                                                                                                                                                                         363 AGTATGATTTGTGCGGGGAACCTTCAGAAGCCCGGATCAGACACCTGCCAGGGTGACTCG 422
                                                                                                                                                                                                                                                                                                                                                                                 423 GGGGGCCCTCTAACCTGTGAGAAGGATGGAACTTACTACGTCTACGGGATTGTAAGCTGG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 GGCCAGGAATGTGGGAAGAAGCCAGGAGTCTACACTCAAGTCACCAAGTTCCTGAATTGG 542
183 TATGTGAAGACTGTATGTTTGCCCAGCGACCCCTTTCCCTCTGGAACTGAGTGCCACATC 242
                                                                                        243 TCTGGCTGGGGTGTTACAGAAACAGGGAAGGGTCCCGCCAGCTCCTGGATGCTAAAGTC 302
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11H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM988 row: e column: 03
High quality sequence stop: 686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1648 ATCAAAGCCACCATCAAAAGTGAAAGTG 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAAGACCACCATGCACAGGGAGGCTG 570

    929
    organism="Mus musculus"

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TITLE
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COMMENT
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FEATURES

Mus musculus (house mouse) Mus musculus BI332440.1 GI:15017097 EST. 481 ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 15 BI332440 LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT 충음 g δ δ /mol_type="miss."...sock.nus /mol_type="missRNA" /strain="C57BL/6J" /db_xref="niasST:B0905008-5" /dbone="NTA:B0809008 IMAGE:30468319" /dev="NTA:B0809008 IMAGE:30468319" /dev=stage="Newborn Kidney" /lab_hots="N1A Mouse Newborn Kidney CDNA Library (Long Email: cdna@lgsun.grc.nia.nih.gov Plate: B0809 row: C column: 08 Seg primer: M13 Reverse High quality sequence stop: 665 POLYA=No. organism="Mus musculus" Location/Qualifiers

GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 360 361 GGCCGGGGCCAATGTCTCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC 420 371 GTCCATGGTGATTGCCTGTAAACAC 430 480 61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCAGACTGGACCCCTGAC 120 77 Grearragaerereaergargreereereeeeeeeeeaaeeeaarragaeeeeeaar 136 121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAACACCAGTAGCACACTTACC 180 137 GACTATIACTACAGCTATGAGCAGTCCAGCCCCAGACGAAGACCCCCAGTGTCAGGCAGACC 196 181 CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC 240 CCCTGTGAACACGGTGGGGACTGCCTCGTCCATGGGAGCACCTTCACATGCAGCTGCCTG 300 1 ATGITTGCCAGGATGTCTGCATGTTCTGCTGTTAATGGCTCTGGTGGGAAAGACA 60 CCTTACACAGGTCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 6; Gaps DB 14; Length 665; 23.7%; Score 399.4; DB 14; Length 76.8%; Pred. No. 1.4e-102; ive 0; Mismatches 146; Indels Query Match Best Local Similarity 76.8' Matches 503; Conservative 241 301 421 면 장 임 qq d g g ð 8 8 ò $\dot{\delta}$

ORIGIN

Nus musculus ambaculus and the transportary Muscaulus and the transportary Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscaes 1 to 791)

Rases 1 to 791)

Rases 1 to 791)

All Dades 1 to 791)

All Institutes of Health, Mammalian Gene Collection (MGC)

All Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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urce /craniality sequence stop: 787.

Location/Qualifiers

urce /craniality sequence stop: 787.

Location/Qualifiers

/clone=InMAGE:5133587"

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40 TOL_CGAP_Li9 Mus musculus CDNA clone IMAGE:5133587 5', mRNA sequence. BI332440 600 610 431 CCTTACACGGGACCAGACTGCTCCAAAGTGCTTCCGGCATGCAGGCCAAACCCCTGCCAG 490 AATGGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCCGAC 491 AATGGCGGAGTCTGTTCCCGACACGGAGATCCAGGTTTACCTGTGCCTGTCCAGAC 541 CAGTICAAGGGGAAATICIGIGAAATAGGIICIGAIGACGCIAIGGIAIGIIGGCGAIGGCIAC 665 FEATURES ORIGIN

Query Match

23.6%; Score 396.4; DB 12; Length 791;
Best Local Similarity 75.6%; Pred. No. 1.1e-101;
Matches 520; Conservative 0; Mismatches 161; Indels 7;

61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCCCAGACTGGACCCCTGAC 120 83 GTCATTGGGCTCTCATGTCCTTCATTGCGCCCCCCAGACCCAGATTGGACCCCGAT 142 121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGAACACCACAGTAGCACACTTACC 180 202 82 143 GACTATTÁCTACAGCTATGAGCAGTCCAGACGAAGACGCCCAGAGACCAGTGTCACGCAGACC 1 ATCTTTGCCAGGATGTCTGATGTTCTGCTGTTAATGGCTCTGGTGAAAGACA 23 a d ò ò ò

Thu May 27 10:53:56 2004

241 CCCTGTGAACACGGTGGGGGCTGCCTCGTCCATGGGGGCACCTTCACATGCAGCTGCCTG 300 257 CCCTGTGAACACGGGGGGACTGTATCATCATGAGGGATACCTTCAGTTGCAGCTGCCCA 316 g ò S B g 장염 8 8 à a δ ò à

Search completed: May 25, 2004, 10:42:53 Job time : 3061 secs

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RESULT I

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VESCULT I

VERSEAL INFORMATION:

PAPLICANT: Takeshi SHIMOWURA et al.

APPLICANT: Takeshi SHIMOWURA et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

APPLICANT: Takeshi SHIMOWURA et al.

TITLE OF INVENTION:

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; LIBRARY: human liver(49, male) cDNA Library (Stratagene)
US-08-148-910-14
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
1.ENGTH: 2033 base pairs
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TYPE: nucleic acid
STRANDEDNESS: double
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IMMEDIATE SOURCE:
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Sequence 9, Appli
Sequence 48, Appli
Sequence 39, Appli
Sequence 1, Appli
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Sequence 58, Appl
Patent No. 5223256
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Sequence 1
Sequence 5
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-448-937A-14
US-08-448-937A-3
US-08-148-910-2
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Sequence 5, Appli Sequence 5, Appli Sequence 64, Appl	Sequence 50, Appl Sequence 54, Appl Sequence 56, Appl Sequence 62, Appl Patent No. 5200340	3 4 4 8 0 3 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Sequence 25, Appl Patent No. 5185259 Patent No. 5185259 Sequence 3, Appli
US-08-558-269-5 US-09-410-882-5 US-08-811-949-64 US-08-811-949-66	US-08-811-949-50 US-08-811-949-54 US-08-811-949-56 US-08-811-949-62 5200340-1		US-08-488-015B-25 5200340-5 5185259-2 US-09-518-046-3
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1738 AACATGCTCTGTGCCGGCTACTT---CGACTGCAAGTCCGACGCTGCCAGGGGGACTCA
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male) cDNA Library (Stratagene)
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/448,937A
FILING DATE: MAY 24, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 56/7164 mber 5, 1993
ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENG/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 500 Kb Storage
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Best Local Similarity 49.6%;
Matches 605; Conservative 0
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SEQUENCE CHARACTERISTICS:
LENGTH: 2033 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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US-08-448-937A-14
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                                       Length 2033,
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                                       Query Match
6.8%; Score 114.4; DB 1;
Best Local Similarity 49.6%; Pred. No. 3.5e-25;
Matches 605; Conservative 0; Mismatches 561;
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CTAGAGACCAGAACTGAAGAAAGAATTCATGAGCAGAGCTTTAGGGTGCAGAAG 1182 1642 AATTGGATCAAAGCCACCAT э : INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE: ORGANISM: hum: IMMEDIATE SOURCE 1123 qq ò 셤 à ò 유 ò 1407 1299 1557 1353 1677 AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACACCTGCCAGGGTGACTCT 1527 GGAGGCCCCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGG 1587 1380 1179 AAGCIGATIGCCAACACTITGIGCAACTCCCGCCAACTCTAIGACCACATGATIGAIGAC 1467 Aacaricricricricciscuacri---caacrecaagrecaacciscoagedagacrea 1794 CCTCTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGCGCTGATCCACCCCTGC 1065 1263 --GCTGGCCGCCATCTACATCGGGACAGCTTCTGCGCCGGGAGCCTGGTCCACACCTGC 1320 TGGGTGCTCACTGCTGCCCCACTGCACCGACATAAAACCAGACATCTAA-----AGGTG 1119 1381 grecregecaceacretroracecaceaceacereacecacereacecacarecacerres 1180 AAGATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCACAATGATATTGCA 1239 1441 AAGTACATCCCGTACACCCTGTACTCCGTGTTCAACCCCAG---CGACCACGACCTCGTC 1497 recenanceer-----encengaenceaecrereseseseseseseseseseseseseseses cercadecadecircecadaceceadacerecadadadadacadadadadadadacerre 1209 1042 rideriectracer---egrepaagakaadacaccercriedaagraktriocogooriegaagdd 1098 eccracracadecradeccccaracciacidecedaarcedaanadaceadadeced 765 TGCTCAGCCCAGGACGTTGCCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTT 885 CCGGGGTTTGACTCCTGTGGAAAGACTGAGATAGCAGAGGAAGAAGATCAAGAGAATCTAT 945 CITIACIGGAACICCCACCICCICITGCAGGAGAATIACAACAIGITIAIGGAGGAIGCI 705 585 802 écchéceceaceagechhégenégacgechéhégaacahéancaagechéanéagegehéchne 861 862 Tradegaacedeargeeracegradegradegradecaecreadecreadecreaderide 921 1498 cicaticadergalagaagaaadgadaecgergrigeeaaagagargargaagaeee TGGGG------TGTTACAGAAACAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC resescencrresarieasaakesreakeeseracreekeekeekeekeekeereere 1678 CCCCTGGTCGCCGACCACAGAGAGAGCCTGAGGTCTACGGCGCGACATCAGCCCC GGAGGCTTTAAGAGCACGGCGAAGCACCCATGGCAGGCGTCCCTCCAGTCCTCGCTG .210 cracescencerarcarcescededrecrectrescreecedescreeners 1120 GTGCTAGGGGACCAGGACCTGAAGAAGAATTTCATGAGCAGAGAGTTTAGGGTGCAG 1240 TIGCTCAAGITAAAGCCAGIGGAIGGICACIGIGCICIAGAAICCAAAIACGIGAAGACI 1300 GIGIGCTIGCCIGAIG-----GGICCTIICCCTCTGGGAGIGAGIGCCACAICTCTGGG cheschesaachesanchechthacassasanscaesachesachesaches -CTGCTAT GAAACCCATGGGATTGGGGAACACAATTTCTGCAGAAACCCCAGATGCGGACGAAAAGCCC TGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAATGGGAATACTGTGATGTCTCAGCC GTTGGCGATGGCTACTCTTACCGAGGGAAAATGAATAGGACAGTCAACCAGCATGCGTGC GCCTGTCCCGACCAGTTCAAGGGGAAATTCTGTGAAATAGGTTCTGATGA 1354 1618 1408 1468 1738 1528 1795 946 1066 1099 1150 1006 586 646 206 982 996 826 886 529 922 qq qq ò 원 상 원 ò 원 ò qq à QQ $\stackrel{>}{\circ}$ 8 8 δ δ S S 8 8 g δ g ò g Sy Dp ò g δ Dþ g ò

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US-08-148-910-3

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Sequence 3, Application US/08148910

Patent No. 54665391

Patent No. 54665391

APPLICANT: Takeshi SHIMOMURA et al.

TILLE OF INVERMION: No. 54665381 Protein and Gene Encoding Said NUMBER OF SEQUENCES: 14

CORRESONDENCE ADDRESS: 14

CORRESONDENCE ADDRESS: 14

CORRESONDENCE SINCH. Lind & Ponack STRATE: 0.5.

COUNTRY: Washington Street, N.W., #700

CITY: Washington Street, S. 25 inch, MEDIUM TYPE: Diskette, S. 25 inch, MEDIUM TYPE: Diskette, S. 25 inch, MEDIUM TYPE: Diskette, S. 25 inch, MEDIUM TYPE: Diskette, S. 25 inch, MEDIUM TYPE: Diskette, S. 25 inch, MEDIUM TYPE: Diskette, S. 25 inch, MEDIUM TYPE: SOUND STORMEN MS-008

COMPUTER: DISKETT, SOUND STORMEN MS-008

SOUTHARRE: Wordperfect

CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: TELECOMMUNICATION INFORMATION: 13,367

REFERENCE DOCKET UNFORMATION: TELEPHONE: 202-371-8856

TELEPHONE: 202-371-8856

INFORMATION: 202-371-8856 1009 CTGACCATCTCCATGCCCCAGGGCCACTTCTGTGGTGGGGGCGCTGATCCACCCTGCTGG 201 criecceccarcracarceseakakaecritcriececekekeccriesreckaecriecries 261 enesnences de celecter de contra 1069 GIGCICACIGCICCACIGCACCGACAIAAAACCAGACA-----TCIAAAGGIGGIG male) 30; Query Match
5.5%; Score 93; DB 1; Length 970;
Best Local Similarity 52.7%; Pred. No. 1.1e-18;
Matches 357; Conservative 0; Mismatches 290; Indels LIBRARY: Pre-made Lambda phage Library, human liver LIBRARY: cDNA Library (Stratagene) GGCCTGGAGTGTGAG--1588

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1183 ATATTCAAGTACAGCCACTACAATGAAAGAGATGAGATTCCCCCACAATGATATTGCATTG 1242
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Patent No. 5677164
GENERAL INPORMATION
TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein NUMBER OF SEQUENCES: 14
CORRESPONDENCE MEDRESS: ADDRESSE: Wenderch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 GECACTTGATGAGAAGGTGAGGGCTACTCCAGCTCCTGCGGGAGGCCCTGGTCCC 617
321 CTGGGCCAGCACTTCTTCAACCGCACGACGACGTGACGCAGACCTTCGGCATCGAGAAG 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498 TGCCTGCCCGAGCCCGGCAGCACCTTCCCCGCAGGACACAAGTGCCAGATTGCGGGCTGG
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MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: SOO KG Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordporfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,937A
FILING DATE: WAY 24, 1995
CLASSIFICATION: 435
PROOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: NO. 5677164ember 5, 1993
ATTONNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 TGGATCAACGACCGGAT 871
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CITY: Washington
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COUNTRY: U.S.A.
ZIP: 20005
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1009 CTGACCATCTCCATGCCCCCAGGGCCACTTCTGTGGTGGGGCGCTGATCCACCCCTGCTGG 1068
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                                                                                                                                                                                                                                                                                                                        Query Match
5.5%; Score 93; DB 1; Length 970;
Best Local Similarity 52.7%; Pred. No. 1.1e-18;
Matches 357; Conservative 0; Mismatches 290; Indels 30; Gaps
                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: Pre-made Lambda phage Library, human liver (49, male)
LIBRARY: cDNA Library (Stratagene)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                  ORGANISM: human
                                                                                                                    linear
                                                                                                             TOPOLOGY: linea
MOLECULE TYPE: CL
ORIGINAL SOURCE:
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TELEFAX: 202-371-8856

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APPLICANT: Takeshi SHIMOMURA et al.
TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STRES: Anderoth, Lind & Ponack STRES: D.C.
COUNTY: Washington STATE: D.C.
COUNTRY: U.S.A.
ZIF: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 gcrinicrichacechicaichedeneneerecechecesececrechaeceee
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4.3%; Score 72.2; DB 1; Length 329;
Best Local Similarity 59.3%; Pred. No. 1.7e-12;
Matches 163; Conservative 0; Mismatches 103; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,910
FILING DATE: No. 5466593ember 5, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 50 KG Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                       GENERAL INFORMATION:
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MOLECULE TYPE: C
ORIGINAL SOURCE:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Takeshi SHIMOMURA et al.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 500 Kb Storage

COMPUTER: IM Compatible

MEDIUM TYPE: MS-DOS

COMPUTER: IM Compatible

COMPUTER: IM SYSTEM: MS-DOS

CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,910
FILING DATE: No. 5465593ember 5, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202-371-8856

13:

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 329 base pairs TYPE: nucleic acid STRANDEDRESS: double

linear

MOLECULE TYPE: CD ORIGINAL SOURCE: ORGANISM: human IMMEDIATE SOURCE: LIBRARY: Quick-c

1440 1441 CAACTCTATGACCACATGATGATGACAGTATGATCTGTGCAGGAAATCTTCAGAAACCT 1500 1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCTGACCTGTGAGAAGGACGGCACC 1560 .s61 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAG-----AAGAGGCCAGGG 1614 168 169 AAGTCCGACGCCTGCCAGGGGACTCAGGGGGGCCCCTGGCCTGCGAGAAGAACGCGTG 228 288 52 recadenceingeadadadeceraciteceeradrecedadeacacaadracadeceer 229 gcrinkcerchacgenhentakerkekengnekekerkekekegeneeneekengekekeke 1381 TOCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGTGCAACTCCCGC 112 gaggicinaceceacateaececeaacaidecicidideceaecit---ceaenec . ა Length 329; Query Match

4.3%; Score 72.2; DB 1; Length 3
Best Local Similarity 59.3%; Pred. No. 1.7e-12;
Matches 163; Conservative 0; Mismatches 103; Indels 1615 GTCTACACCCAAGTTACCAAATTCCTGAATTGGAT 1649 Grenacacecerecechaciangidadenican 323 US-08-148-910-13 RESULT 7 US-08-448-937A-2 g 셤 g ò d ò ò ઠે

> RESULT 6 US-08-148-910-13 ; Sequence 13, Application US/08148910

Quick-cloneTM human liver cDNA (Clonetech)

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Patent No. 567164

Patent No. 567164

GENERAL INFORMATION:

APPLICANT Takeshi SHIMOMURA et al.

TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Frotein

TITLE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein

TUTRE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein

TUTRE OF INVENTION: No. 5677164el Protein and Gene Encoding Said Protein

TORRESPONDENCE: 110 & Ponack

STREET: 05 SILteenth Street, N.W., #700

STREET: 805 Filteenth Street

COUNTRY: 10.S.A.

ZIP: 2000s

COUNTRY: 10.S.A.

SOFTWARE: SOO & Streage

COMPUTER: 1BM Compatible

OPERATION TYPE: 10508

SOFTWARE: Way 24, 1056

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 105/08/448,937A

FILING DATE: NA 245

FILING DATE: NA 245

FILING DATE: NA Cheek, Jr.

RESISTRATION NUMBER: 3, 367

REFERENCE/DOCKET NUMBER:

TELECOMMUTCATION INFORMATION:

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TELECOMMUTCATION INFORMATION:

TELEFAX: 202-371-8850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 gcrihaccichhaddedichtentehaddigadagacdacidedadagactachahadadadda 288
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4.3%; Score 72.2; DB 1; Length 329;
Best Local Similarity 59.3%; Pred. No. 1.7e-12;
Matches 163; Conservative 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quick-cloneIM human liver cDNA (Clonetech)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 319 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: human
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LIBRARY: Quick
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1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCTGACCTGTGAGAAGGACGGCACC 1560
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Sequence 13, Application US/08448937A

Sequence 13, Application US/08448937A

Patent No. 5677164

GENERAL INFORMATION:

APPLICANT Takeshi SHIMOMURA et al.

ATTLE OF INVANTION: No. 5677164el Protein and Gene Encoding Said Protein
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSE: Wenderoft, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D.C.

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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IMMEDIATE SOURCE:
LIBRARY: Quick-cloneTM human liver cDNA (Clonetech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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Best Local Similarity 59.3%; Pred. No. 1.7e-12;
Matches 163; Conservative 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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CURRENT APPLICATION DATA:
PEDILOGION NUMBER: US/08/448,937A
PILING DATE: May 24, 1995
CLASSIFICATION: 435
PROG APPLICATION DATA:
APPLICATION NUMBER: 08/148,910
FILING DATE: No. 5677164ember 5, 1993
ATTONREY/ABORT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 i
MEDIUM TYPE: 500 KD Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect
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SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-8856
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FRY: U.S.A.
20005
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RESULT 8

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us-09-912-559-2.rni

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RESULT 10
US-08-427-640-5
I Sequence 5, Application US/08427640
| Sequence 5, Application US/08427640
| Patent No. 5658788
| GENERAL INFORMATION:
| APPLICANT: Berg et al.
| TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor NUMBER OF SEQUENCES: 28
| OKRESPONDENCE ADDRESS: 28
| ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center | CITY: Indianapolis | STATE: IN. | COUNTRY: U.S.A.
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866 CTCGGAGGCGCGCCCAGGCAAACTTGCACGACGCCTGCCAGGCGATTCGGAGGCC
                                                                                                                                                                                                                                                                 986 GCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAGGTTACCAACTACCTAGACTGGA
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                                                                                             CCCTGACCTGTGAGAAGGACGGCACCTACTACGTCTATGGGATAGTGAGCTGGGGCCTGG
                                                                                                                                          926 CCCTGGTGTGTGTACGATGGCCGCATGACTTTGGTGGGCATCACAGCTGGGGCCTGG
                                                                                                                                                                                                                        1595 AGIGTGAGAAGAGG-----CCAGGGGTCTACACCCAAGITACCAAATTCGAA
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COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,640
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/689,4:
FILING DATE: 22 APRLE 1991
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYRE: RUCLAIG CAIG
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                               1649 TCAAAGCCACCAT 1661
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; MOLECULE TYPE:
US-08-427-640-5
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                                                      Sequence 1, Application US/08427640

Patent No. 5658788
GENERAL IMPROMATION:
APPLICANT: Berg et al.
TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Inliny and Company
STREET: Indianapolis
STATE: IN.
COUNTRY: U.S.A.
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Pred. No. 3.7e-12;
0; Mismatches 288; Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage
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                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,640
FILLING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/689,41
FILING DATE: 22 APRLL 1991
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.5%;
Matches 340; Conservative (
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MOLECULE TYPE: DNA
US-08-427-640-1
                RESULT 9
US-08-427-640-1
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RESULT 12
US-09-553-498-9
Sequence 9, Application US/09553498
Sequence 9, Application US/09553498
Sequence 9, Application US/09553498
Sequence 9, Application US/09553498
APPLICANT: Rudolph, Rainer
APPLICANT: Schwarz, Elisabeth
TILE OF INVENTION: Process for the production of naturally folded and secreted protrings number: Case 20379
CURRENT FILING DAIE: 2000-04-20
SEROID NOS: 10
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NOS: 10
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US-09-553-498-9
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Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NAINO, YOSHIMASA
APPLICANT: SAJAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: HOYANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
APPLICANT: NOTANI, JOUJI
IIILE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                            4.3%; Score 72.2; DB 4;
50.5%; Pred. No. 3.8e-12;
cive 0; Mismatches 288;
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Best Local Similarity 50.5<sup>3</sup>
Matches 340; Conservative
                                                  coli
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Escherichia cc;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1137)
US-09-618-869-9
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US-08-811-949-48
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Parent No. 645529

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APPLICANT: Rudolph, Rainer

APPLICANT: Schwaffer, Joerg

APPLICANT: Schwaffer, Joerg

APPLICANT: Schwaffer, Joerg

APPLICANT: Schwaffer, Joerg

APPLICANT: Schwaffer, Joerg

APPLICANT: Schwaffer, Joerg

APPLICANT: Schwaffer, Joerg

TITLE OF INVENTION: GRAPERONES

FILE SPERENCE: 2008

CURRENT PLLING DATE: 2000-07-19

FRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9
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                                                                                                          AGGGCCACTICTGTGGGGGGGGGCGTGATCCACCCCTGCTGGGTGCTCACTGCTGCCCACT
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          Length 1137;
          Score 72.2; DB 4; Length 1
Pred. No. 3.8e-12;
0; Mismatches 288; Indels
       Query Match
Best Local Similarity 50.5%;
Matches 340; Conservative
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1163 GCTTCCAGGAGGTTTCCGCCCCACCTGACGGTGATCTTGGGCAGAACATACCGGG 1222 1292 TTCGTGACACAT 1304 LENGTH: 1955 base pairs 1649 TCAAAGCCACCAT 1661) ORGANISM: Homo sapiens US-08-883-795A-39 TYPE: nucleic acid STRANDEDNESS: single 1490 TTCAGAAACCTGG linear MOLECULE TYPE: ORIGINAL SOURCE: US-08-883-795A-39 q ò QQ ò g ò D. g $\stackrel{>}{\delta}$ CAGGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTCAAGCTGATTGCCAACACTTTGT 1429 1430 GCAACTCCCGCCAACTCTATGACCACATGATGATGACAGTATGATCTGTGCAGGAAATC 1489 1052 GCACATCACAACATTAACTTAACAGAACAGTCACGGACAACATGCTGTGTGCTGGAGACA 1111 1141 1202 ACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261 1028 AGGGCCACTICTGTGGTGGGGGCGCTGATCCACCCCTGCTGGGTGCTCACTGCTGCCCCACT 1087 1142 AGAAAGAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCACT 1201 818 TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCTGCAGCTGAAATCGGATT 871 CGTCCCGCTGTGCCCAGGAGAGAGCAGCGTGTCGGACTGTGTGCCTTCCCCCGGGGACC 931 697 698 écrrecaggaggrirecgecéceacéacérgacgrigarerregécagaacaracdege 757 1088 GCACCGA-----CATAAAACCAGACATCTAAAGGTGGTGGTAGGGGACCAGGACCTGA 992 crecrrreraricesascescreaaseskeerearsicascreteraecearecaecr 758 TGGTCCCTGGCGAGGAGGAGCAGAATTTGAAGTCGAAAATACATTGTCCATAAGGAAT 638 AGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTCTGCCGCCCCCT Gaps 45; NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
ADDRESSEE: P.C.
CITY: ARLINGTON
CITY: ARLINGTON
CITY: USA
COUNTRY: USA
ZIP: 2222
ZIP: COMPUTER FRADABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: ISW PC COMPALIBLE
COMPUTER: ISW PC COMPALIBLE
COMPUTER: DEAGHIN PREJECTION DITA:
APPLICATION DITA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 09-MAR-1997
CLASSIFICATION: NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 24,618
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REPRENCE/DOCKET NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 24,618
REPRENCE/DOCKET NUMBER: 18-966-0
TELEFONDUNICATION INFORMATION:
TELEFAX: 703-413-3000
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTER STICS:
LENTH: 1134 Dase pairs Length 1314; Score 72.2; DB 2; Length 13 Pred. No. 4.2e-12; 0; Mismatches 288; Indels TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) Query Match Best Local Similarity 50.5%; Matches 340; Conservative nucleic acid EDNESS: double 1..1311 NAME/KEY: CDS STRANDEDNESS: , LOCATION: US-08-811-949-48 872 1322 a à g ò 8 D ò g $\dot{\delta}$ d à d δ

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4.3%; Score 72.2; DB 2; Length 19:
Best Local Similarity 50.5%; Pred. No. 5.4e-12;
Matches 340; Conservative 0; Mismatches 288; Indels
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ZONTRY: Canada

ZONTRY: Canada

ZONPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT AFPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLESSIFICATION: 40-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
REFERENCE/DOCKET NUMBER: 7841-062
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1595 AGTGTGAGAAGAGG-----CCAGGGGTCTACACCAAGTTACCAAATTCCTGAATTGGA 1648
1697 GCTGTGGACAGAAGGATGTCCCGGGTGTGTACCAAGGTTACCAAGTTACCAAGCTGGA 1756
                                                                                                                                                                                                                                                           1457 CICCITICIAITICGGAGCGGCTGAAGAGCTCAIGTCAGAACTGTACCCAICCAGCCGCT 1516
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                    1283 TCGAT-----GATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAATCGGATT 1336
                                                                                                                                    1322 TTCCCT------CTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAA 1369
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                                                        1202 ACAATGAAAGAGATGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTGG 1261
                                                                                                                 1262 ATGGTCACTGTGCTCTAGAATCCAAATACGTGAAGACTGTGTGCTTGCCTGATGGGTCCT 1321
1142 AGAAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCACT 1201
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Search completed: May 25, 2004, 10:46:20 Job time : 96.5 secs

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May 25, 2004, 09:00:39 ; Search time 528.5 Seconds (without alignments)
14472.614 Million cell updates/sec
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1683
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| cgn2_6/prodata/2/pubpna/US07_puBCOMB.seq:*
| cgn2_6/prodata/2/pubpna/DS06_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 4, Appli		Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1668, Ap	Seguence 8242, Ap	Sequence 17, Appl	Sequence 11164, A	Sequence 27791, A	Sequence 552, App	Sequence 1612, Ap	Sequence 590, App
ΠD	US-09-912-559-2	US-10-391-215-4	US-10-391-215-2	US-10-391-215-3	US-09-912-559-1	US-10-391-215-1	US-09-880-107-1668	US-09-918-995-8242	US-10-425-000-17	US-09-864-761-11164	US-09-864-761-27791	US-09-954-456-552	US-09-880-107-1612	US-10-087-192-590
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Query Match Length DB	1683	1683	1683	1683	1683	1683	3008	428	264	451	117	2036	2036	1302
Query	100.0	100.0	6.66	99.9	99.8	99.66	8.66	21.9	15.6	7.1	7.0	6.8	6.8	5.5
Score	1683	1683	1681.4	1681.4	1679.8	1679.8	1679.8	368.4	262.4	120.2	117	114.4	114.4	93.2
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5-216-10	US-10-027-632-17496	US-10-027-6	- 7	9-969-27	37-2	US-10-411-026-25	62-2	17 US-10-411-049-25	US-10-342-887-541	US-10-172-118-541	US-10-193-656-7	US-09-969-271-5	US-10-342-887-540	US-10-172-118-540	70	US-09-974-298-144	US-09-814-353-19992	-09-987-	US-09-987-455-7	-09-987-455	US-09-987-455-5	-11	-10-004-113	US-10-004-113-56	US-10-152-319A-2167	09-814-353-14	US-10-159-563-132	-10-247-671	US-10-116-802-163	US-09-898-837A-16
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ALIGNMENTS

GAPLICANT: ROBERSON:

APPLICANT: ROBERSON:

APPLICANT: STOCHER, HANS-ARNOLD

APPLICANT: FEUSENBER, HANS-ARNOLD

APPLICANT: FEUSENBER, HANS-ARNOLD

APPLICANT: LANG, WIEGAND

APPLICANT: LANG, WIEGAND

APPLICANT: LANG, WIEGAND

APPLICANT: MERINER, THOMAS

APPLICANT: NERLINGL CLAUDIA

APPLICANT: NERLINGL CLAUDIA

APPLICANT: NERLINGL MERINGERIT

APPLICANT: NERLINGL MERINGL STORE

APPLICANT: NUMBERS: US/09/912,559

CURRENT PELLING DATE: 2000-07-26

PRIOR PILING DATE: 2000-07-26

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2001-07-26

PRIOR PELLORION NUMBER: DE 100 50 040-4

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2001-07-21

NUMBER OF SEQ ID NOS: 4

SOFTWARER: PALENTIN NUMBER: DE 10 52 319-6

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 4

SOFTWARER: PALENTIN VEY: 2.1

SSP ID NO 2

LENGTH: NANA Length 1683; Query Match 100.0%; Score 1683; DB 9; Best Local Similarity 100.0%; Pred. No. 0; Matches 1683; Conservative 0; Mismatches 0; Sequence 2, Application US/09912559 Patent No. US20020142316Al GENERAL INFORMATION:

QY 1081 GCCCACTGCACCGACATAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG 1140 Db 1081 GCCCACTGCACATAAAAACCAGACATCTAAAGGTGGTGCTAGGGGACCAGGACCTG 1140	QY 1141 AAGAAAGAATTTCATGAGCAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCAC 1200 Db 1141 AAGAAGAATTTCATGAGCAGGCTTTAGGGTGCAGAAGATATTCAAGTACAGCCAC 1200	QY 1201 TACAATGAAAGAGATTCCCCACAATGATATTGCATTGCTCAAGTTAAAGCCAGTG 1260	GAIGGICACTGIGCTCIAGAAICCAAAIACGIGAAGACTGIGTGCTIGCCIGAIGGGICCCCAAIGGICCCGAIGGGICCCGAIGGGICCCGAIGGGICCCGAIGGICCCGAIGGGICCCGAIGGGICCCGAIGGICACGAAIACGIGAAGACIGIGCTIGCCIGAIGGGICC	Oy 1321 TITCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGGTGTTACAGAAACAGGAAAAGGG 1380 Db 1321 TITCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGTGTTACAGAAACAGGAAAAGGG 1380		OY 1441 CAACTCTATGACCACATGATTGATGACGAGTATGATCATCAGGAAATCTTCAGGAAACCT 1500 Db 1441 CAACTCTATGACCACATGATGACGAGTATGATGATCATGCAGGAAATCTTCAGAAACCT 1500	Oy 1501 GGGCAAGACACCTGCCAGGGTGACTCTGGAGGCCCCTGACCTGTGAGAAGGACGGCACC 1560	Qy 1561 TACTACGTCTATGGGATAGTGAGCTGGGGCCTGGAGTGTGAGAAGAGGCCAGGGGTCTAC 1620	1621 ACCC 1 1621 ACCC	CY 1681 TAA 1683 Db 1681 TAA 1683	RESULT 2 US-10-391-215-4 ; Sequence 4, Application US/10391215	; PUDICATION NO. USZUG40009543A1 ; GENERAL INFORMATION: ; APPLICANT: KIECHL, STEFAN ; APPLICANT: WILLEIT, JOHANN	APPLICANT: ROEMISCH, UGSEF, APPLICANT: ROEMISCH, UGSEGN APPLICANT: WEIMER, THOMAS APPLICANT: FEUSSNER, ANNETTE	; APPLICANT: DOERSAM, VOLKER ; APPLICANT: DOERSAM, VOLKER ; TITLE OF INVENTION: MARBURG I MUTANT OF FACTOR VII ACTIVATING PROTEASE ; TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS	; FILE REPRENCE: 06478.1457-01 ; CURRENT APPLICATION NUMBER: 05/10/391,215 ; CURRENT FILING DATE: 2003-03-19 ; PRIOR APPLICATION NUMBER: 09/912,559	FRIOR FILING DATE: 2001-07-26 PRIOR APPLICATION NUMBER: DE 100 36 641.4 PRIOR FILING DATE: 2000-07-26 PRIOR APPLICATION NUMBER: DE 100 50 040.4	; FRIOR FILING DATE: 2000-10-10 ; PRIOR APPLICATION NUMBER: DE 100 52 319.6 ; PRIOR FILING DATE: 2000-10-21 ; PRIOR APPLICATION NUMBER: DE 101 18 706.8 ; PRIOR FILING DATE: 2001-04-12
Qy 1 AIGTITGCCAGGATGTCTGATCTCCATGTTCTGCTTAATGGCTCTGGTGGGAAGACA 60 Db 1 ATGTTTGCCAGGATGTCTGATCTCCATGTTCTGTTAATGGCTCTGTTGGGAAAGACA 60	61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGGACCTGACCTGACCTGACCCCTGAC 61 GCCTGTGGGTTCTCCCTGATGTCTTTATTGGAAAGCCTGAACCAGACCAGACCGAACCCTGACCTGAAGCCTGGACCTGAAGCCTGGACCTGGACCTGGACCTGGACCTGGACCTGGACCCTGAAGCCTGGACCCTGAAGCCTGGACCCTGACCTGACACCTGACACCTGACACCTGACCTGACACACAC	121 CAGTATGATTACAGCTACGAGGATTATAATCAGGAAGAGACACGAACGA	181 CATGCTGAGAATCCTGACTGCTACTGAGGACCAAGCTGATCCATGCCAAGCTACATGCTAACTGACAAGCTAACTGAATCCTAACTGAATCCTGAACTGACTAACTGAGAACCTGAATCCATGCCAAGCTAACTGAATCCTAACTAA	241 CCCTGTGAACACGGTGGGAACTGCTCGTCCATGGGAGCACCTTCACATGCAGC 	301 GCTCCTTTCTCTGGGAATAAGTGTCAGAAAGTGCAAAATACGTGCAAGGACAACCCATGT 	361 GGCCGGGCCCAATGTCTCATTACC	Oy 421 CCTTACACAGATCCCAGCTGCTCCCAAGTGGTTCCTGTATGCAGGCCAAACCCCTGCCAG 480	481 AATGGGCTACCTGCTCCCGGCATAAGCGGAGATCCAAGTTCACCTGTGCCTGTCCCGACTTCACTGTGCCTGTCCCGGCGAAACCGGAGAATCCAAGTTCACCTGTGCCTGTCCCGGC	541 CAGTTCAAGGGAAATTCTGTGAAATAGGTTCTGATGAC 	OY 601 TCTTACCGAGGAAAATGAATAGACAGTCAACCAGCATGCGTGCCTTTACTGGAACTCC 660	Oy 661 CACCICCTCTTGCAGGAATTACAACATGTTTATGGAGGATGCTGAAACCCATGGGATT 720	OY 721 GGGGAACACAATTTCTGCAGAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTTATTAAA 780 Db 721 GGGGAACACAATTTCTGCAGAAAACCCAGATGCGGACGAAAAGCCCTGGTGCTTATTAAA 780	OY 781 GTTACCAATGACAAGGTGAAATGGGGAATACTGTGATGTCTCAGCCTGCTCAGCCCAGGAC 840	OY 841 GITGCTACCCAGAGGAAAGCCCCACTGAGCCATCAACCAAGCTTCCGGGGTTTGACTCC 900	OY 901 TGTGGAAAGACTGAGAAGAGGAAGATCAAGAGAATCTATGGAGGCTTTAAGAGC 960 	OY 961 ACGGGGGGAAGCACCCATGGCAGGGTCCCTCCAGTCCTCGGCTGCCTCTGACCATCTCC 1020	OY 1021 AIGCCCCAGGGCCACTTCTGTGGTGGGGGGGGGGTGATCCACCCTGCTGGGGGGTGTACTGCT 1080

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NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. SEQ ID NO 4 sapiens TYPE: DNA CRGANISM: Homo US-10-391-215-4 LENGTH: 1683

Gaps 1683; ö Length Indels 16; . 0 В 0; Mismatches 100.0%; Score 1683; 100.0%; Pred. No. 0; Query Match Best Local Similarity 100. Matches 1683; Conservative 8 8

TACAATGAAAGAGATGAGATTCCCCACAATGATATGCATTGCTCAAGTTAAAGCCAGTG

GCCCACTGCACCGACATAAAAACCAGACATCTAAAAGGTGGTGCTAGGGGACCAGGACCTG

AAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGCAGAAGATATTCAAGTACAGCAA

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CATGCTGAGAATCCTGACTGGTACTACACTGAGGACCAAGCTGATCCATGCCAGCCCAAC

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RESULT 3

US-10-391-215-2

| Sequence 2, Application US/10391215
| Sequence 2, Application No. US20040009543A1
| GENERAL INFORMATION:
| APPLICANT: KIECHL, STEPAN
| APPLICANT: WILLEIT, JOHANN
| APPLICANT: WIEDERMANN, CHRISTIAN JOSEF
| APPLICANT: REMER, THOMAS
| APPLICANT: STORME, THOMAS
| APPLICANT: STORME, HANS-ARNOLD
| APPLICANT: STORME, HANS-ARNOLD
| APPLICANT: DOERSAM, VOLKER
| TITLE OF INVENTION: MARBURG I MITANT OF FACTOR VII ACTIVATING PROTEASE
| TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
| FILE REFERENCE: 064-18.1457-01
| CURRENT APPLICATION NUMBER: US/10/391,215

TAA 1683

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CURRENT FILING DATE: 2003-03-19
PRIOR APPLICATION NUMBER: 09/912,559
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-10-10
PRIOR PILING DATE: 2000-10-10
PRIOR PILING DATE: 2000-10-11
PRIOR PLING DATE: 2001-0-11
PRIOR PILING DATE: 2001-0-21
PRIOR PILING DATE: 2001-0-21
PRIOR PILING DATE: 2001-0-11
PRIOR PILING DATE: 2001-0-11
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12 j LENGTH: 1683 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-391-215-2

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ö Gaps Length 1683; ; 0 1; Indels DB 16; Score 1681.4; 1; Pred. No. 0; 0; Mismatches Query Match Best Local Similarity 99.9%; Matches 1682; Conservative C

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RESULT 4
US-10-391-215-3
Sequence 3, Application US/10391215
Publication No. US20040009543A1
GENERAL INFORMATION:
APPLICANT: KIECHL, STEFAN

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APPLICANT: WILLEIT, JOHANN
APPLICANT: WIEDERNANN, CHRISTIAN JOSEF
APPLICANT: WIEDERNANN, CHRISTIAN JOSEF
APPLICANT: ROMISCH, JUERGEN
APPLICANT: ROMISCH, JUERGEN
APPLICANT: PRUSSNER, THOMAS
APPLICANT: PRUSSNER, ANNETE
APPLICANT: STOEHR, HAMS-ARNOLD
APPLICANT: STOEHR, HAMS-ARNOLD
APPLICANT: STOEHR, HAMS-ARNOLD
APPLICANT: STOEHR, HAMS-ARNOLD
APPLICANT: STOEHR, HAMS-ARNOLD
APPLICANT: STOEHR, HAMS-ARNOLD
APPLICANT: OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
CURRENT APPLICATION NUMBER: US/10/391,215
CURRENT APPLICATION NUMBER: DE 100 50 040.4
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 8 -04-12
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NUMBER OF SEQ ID NOS: 8 -04-14-14
NUMBER OF SEQ ID NOS: 8 -04-14-14
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Sequence 1, Application US/09912559

Patent No. US20020142316A1

GENERAL INFORMATION

APPLICANT STORER, HANS-ARNOLD

APPLICANT STORER, HANS-ARNOLD

APPLICANT FEUSINER, ANNETTE

APPLICANT WEINER, THOMAS

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TITLE OF INVENTION WHERE: US/09/912,559

CURRENT APPLICATION WHERE: DE 100 36 641.4

PRIOR FILING DATE: 2000-07-26

PRIOR FILING DATE: 2000-10-10

PRIOR FILING DATE: 2000-10-10

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 1

LEADTH: 1683

LEADTH: 1683
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Oy 1561 TACTACGTCTATGGGATAGTCGGCCTCGGACTCTGAGAGGGCCCAGGGGTCTAC 1620 Db 1561 TACTACGTCTATGGGATAGTCGGCCTCGGAGTGTGGGGAGGCCCAGGGGTCTAC 1620 Oy 1621 ACCCAAGTTACCAAATTCCTGAATCGAGTCATCAAAGTGAAAGTGGAAAGTGGATCT 1680 Db 1621 ACCCAAGTTACCAAATTCCTGAATTGGATCAAAGCCACCATCAAAAGTGAAAGTGGCTTC 1680	1681 TAA 1683 1681 TAA 1683	RESULT 6 US-10-391-215-1	Sequence 1, Application 05/10394115 Chublication No. US20040009543A1 GENERAL INFORMATION: APPLICANT: KIECHL, STEFAN	, APPLICANT: WILLEIT, JOHANN , APPLICANT: WIEDERMANN, CHRISTIAN JOSEF , APPLICANT: ROEMISCH, JUERGEN , APPLICANT: WEIMER, THOMAS	APPLICANT: FEGSSNER, ANNETTE APPLICANT: STOCHE, HANS-ARNOLD TAPPLICANT: DORRSAM, VOLKER TITLE OF INVENTION: MARBURG I MUTANT OF FACTOR VII ACTIVATING PROTEASE	TITLE OF INVENTION: (FSAP) AS RISK FACTOK FOR ARTERIAL THROMBOSIS; FILE CURRENT APPLICATION NUMBER: US/10/391,215; CURRENT FILING DATE: 2003-03-19	PRIOR APPLICATION NUMBER: 09/912,559 PRIOR FILING DATE: 2001-07-26 PRIOR APPLICATION NUMBER: DE 100 36 641.4 PRIOR FILING DATE: 2000-07-26	; PRIOR APPLICATION NUMBER: DE 100 50 040.4 ; PRIOR FILING DATE: 2000-10-10 ; PRIOR FILING DATE: 2000-10-21 ; PRIOR FILING DATE: 2000-10-21	PRIOR APPLICATION NUMBER: DE 101 18 706.8 PRIOR FILING DATE: 2.001-04-12 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.1	; SEQ ID NO 1 ; LENGTH: 1683 TYPE: DNA ; ORGANISM: Homo sapiens	OS-IU-391-215-1 Query Match Query Match Sest Local Similarity 99.3%; Pred. No. 0; Matchee 1691. Concernative 0. Minaatches 2: Indels 0: Gabs 0:	TITIGCCAGGATGTCTGATGTTCGCTGTTAATGGCTTGGTGGGAAAGACA 60	ccreac 1	121 CAGIAIGAITACAGCIACGAGAITAIAATCAGGAAGAGAGACACCAGIAGCACATTACC 1	CATGCTGAGAATCCTGACTGACTGACGACCCAAGCTGATCCATGCTGCCCCCAC 24	241 CCCTGTGAACACGGTGGGGACTGCCTCGTCGAGGGACCTTCACATGCAGCTGCCTG 241 CCCTGTGAACACGGTGGGACTGCTCATGCAAGAACAACAAGAAGTGCTG 241 CCCTGTGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

					541 CAGITCAAGGGGAAATI 	601 TCTTACCGAGGAAAAT 	661 CACCTCCTCTTGCAGGA 	721 GGGGAACACAATTTCTG	781 GTTACCAATGACAAGGT	87) GIIACCAALGACAGGG	937 GTTGCCTACCCAGAGGE 901 TGTGGAAAGACTGAGAT	997 TGTGGAAAGACTGAGAT 961 ACGGCGGGCAAGCACCC 1057 ACGGCGGGAAGCACCC		1081	1141 1237 1237	1297	1261	1321 TTTCCCTCTGGGGACTG
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            TCATTACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAACACCCTGTATAACACCTGTATACCCAGAGTCCTCCCTACTACCGCTGTGTCTGTAAACAC
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RESULT 10
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1417 ITTCCCTCTGGGAGTGAGTGCCACATCTCTGGCTGGGGTGTTACAGAAACAGGAAAAGGG 1476
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21.9%; Score 368.4; DB 10; Length
Best Local Similarity 99.7%; Pred. No. 4.1e-111;
Matches 369; Conservative 0; Mismatches 1; Indels
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CORGANISM: Homo sapiens
US-09-918-995-8242
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OTHER INFORMATION: Nucleotide sequence encoding the kringle domain of the hyaluronan CHER INFORMATION: binding protein US-10-425-000-17
                                                                                                                                                                                                US-10-425-000-17

Sequence 17, Application US/10425000

Sequence 17, Application US/10425000

Sequence 17, Application US/10425000

Sequence 17, Application William Sequence 17, Application William Sequence 17, Applicant Neabit, Mark

APPLICANT: Cameron, Beatrice

APPLICANT: Blanche, Francis

TITLE OF INVENTION: Aringle Polypeptides and Methods for Using Them to Inhibit

TITLE OF INVENTION: Anglogenesis

TITLE OF INVENTION: Anglogenesis

TITLE OF INVENTION: Anglogenesis

TITLE OF INVENTION: Anglogenesis

TITLE OF INVENTION: Anglogenesis

TITLE APPLICATION NUMBER: US/10/425,000

CURRENT APPLICATION NUMBER: 10/233,675

PRIOR FILING DATE: 2002-09-04

NUMBER OF SEQ ID NOS: 105

SOFTWARE: Patentin version 3.2

LENGARISM: Artificial Sequence

FRANISM: Artificial Sequence

FRANISM: Artificial Sequence
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| Sequence 11164, Application US/09864761
| Sequence 11164, Application US/09864761
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharin G.
| APPLICANT: Rank, David R.
| APPLICANT: Hanzel, David K.
| APPLICANT: HANZEL DAVID WENSHARD SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILLS REPRESTORS: AGOMICA-X-1
| FILLE REPRESTORS: AGOMICA-X-1
| CURRENT APPLICATION NUMBER: US/09/864,761
| CURRENT FILLING DATE: 2001-05-23
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Best Local Similarity 99.6%; Pred. No. 5e-76;
Matches 263; Conservative 0; Mismatches 1; Indels
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APPLICANT: REAL SEATION AND THE STATES AND ADDRESS USEFUL FOR TITLE OF INVENTION: GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GRANK GR
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INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
INFORMATION: EXPRESSED IN BOLT LIVER, SIGNAL = 2.9
INFORMATION: WISSPROY HIT: Q25464, EVALUE 1.00e-03
INFORMATION: STILHWAN HIT: TE86661, EVALUE 7.00e-55
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.0

US-09-864-761-11164
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-00-03
PRIOR PILING DATE: 2000-00-04
PRIOR FILING DATE: 2000-00-04
PRIOR FILING DATE: 2000-00-07
PRIOR FILING DATE: 2000-09-27
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Best Local Similarity 97.6
Matches 122; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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391 117 rechaharakerechaesakerenteresekesekerekarerentarakerekakakere se 332 TGCAAAATACGTGCAAGGACAACCCATGTGGCCGGGGCCAATGTCTCATTACCCAGAGTC Gaps ö Length 117; 7.0%; Score 117; DB 9; L 100.0%; Pred. No. 6.2e-28; tive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 117; Conservative US-09-864-761-27791 g à

RESULT 11 2.09-864-761-27791,c ; Sequence 27791, Application US/09864761 ; Patent No. US20020048763A1

444 CCAAG 448 CCAAG 327

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1102 IGCGAATCCCTCACCAGAGTCCAACTGTCACGGATCTCCTGGCGACCTG	Db 1153 CCTGAGGGGGCCCCGGGGGCCCAGGCCAGGCAGGAGGAGAAGA	Db 1213 CTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	s Using Cand Qy 1006	Qy 1066 TGGGTGCTGCCGACATGGACATAAAAACCAGACATCTAAAGGTG	Qy 1120 GTGCTAGGGACCTGAAGAAAGAATTTCATGAGCAGAGCTTTAGGGTGCAG	Qy 1180 AAGATATTCAAGTACAGCCACTACAATGAAAGAGATTGCCCACAATGATATTGCA	2y 1240 TIGCTCAAGTTAAAGCCAGTGGATGGTCACTGTGCTCTAGAATGCGAAATACGTGAAGACT	Qy 1300 GIGIGCITGCCIGAIGGGICCITTCCCICIGGAAGIGAGIGCCACAICITGGC 	Qy 1354 TGGGGTGTTACAGAAACAGAAAAGGGTCCCGCCAGCTCCTGGATGCCAAAGTC	Qy 1408 AAGCTGATTGCCAACACTTTGTGCAACTCCGGCGAACTCTATGACTGATTGAT	Oy 1468 AGTATGATCTGTGCAGGAAATCTTCAGAAACCTGGGCAAGACCTGCCAGGGTGACTCT	10; Qy 1528 GGAGGCCCCTGAACTGTGAGAAGGACGGCACCTACTATGGGATAGTGAGCTGG [BU4 QY		705 984 765	A APPLICANT: HOCKLEY, JOSEPH G. 7 APPLICANT: Scherf, Uwe 7 APPLICANT: Scherf, Uwe 825 / APPLICANT: Gane Logic, Inc. 7 TTTE OP INTERMEDIAL Cana Broffiles in Liver Cancer	מפפרסוו בדסדודעם זוו חדיעני כשווי
Oy 392 CTCCCTACTACTACTGTCTGTAAACACCCCTTACACAGGTCCCAGCTGCTCCCAAG 44:	SULT 12	US-09-954-456-552 ; Sequence 552, Application US/09954456 ; Patcent No. US-20115057A1 ; GENERAL INFORMATION:	APPLICANT: Young, Paul TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agent TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76	CURRENT APPLICATION NUMBER: US/09/954,456 CURRENT FILING DATE: 2001-09-18 PRIOR APPLICATION NUMBER: US/60/233,617 PRIOR FILING DATE: 2000-09-18	PRIOR APPLICATION NUMBER: US/60/234,052 PRIOR FILING DATE: 2000-09-20 PRIOR APPLICATION NUMBER: US/60/234,923 PRIOR FILING DATE: 2000-09-25	PRIOR APPLICATION NUMBER: US/60/235,134 PRIOR FILING DATE: 2000-09-25 PRIOR APPLICATION NUMBER: US/60/235,637 PRIOR FILING DATE: 2000-09-26	PRIOR APPLICATION NUMBER: US/60/235,638 PRIOR FILING DATE: 2000-09-26 PRIOR APPLICATION NUMBER: US/60/235,711 PRIOR PILING DATE: 2000-09-27	PRIOR APPLICATION NUMBER: US/60/235,720 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US/60/235,840 PRIOR FILING DATE: 2000-09-27	PRIOR APPLICATION NUMBER: US/60/235,863 PRIOR FILING DATE: 2000-09-27 NUMBER OF SEQ ID NOS: 2276 SOFTWARE: Patentin version 3.0	없그단이	456-552 atch cal Similarity 49.6%; Pred. No. 2.5e-26;	Matches 605; Conservative 0; Mismatches 561; Indels 54; 469 AACCCTGCCAGAATGGGGTACCTGCTCCCGGCATAAGCGGAGATCCAAGTT	VD /45 AGCCCTIGCCTGACGGGGGGAATTCTGTGATGGTGACCACGGGAACCACGGGAACCACGGGGACCACGGGGAACAATTCTGTGAAATAGGTTCTGATGAACTGAATTCTGATGAAATAGGTTCTGATGAACTAATAGGTTCTGATGAAATAGGTTCTGATGAATAGGTTCTGATGAATAGAATAGAATAGAATAGAATAGAAATAGAAATAGAAAATAGAAAATAGAAAATAGAAAATAGAAAATAGAAAATAGAAAAAA	S86 GTTGGCGATGGCTACTTACCGAGGGAAATGAATAGGACAGTCAACCAGGAGAATGAAT	QY 646 CITIACIGGAACTCCCACCTCCTCTTGCAGGAGAATTACAACATGTTTATGGAGGATGCT Db 925 CTGGCTGGAACTCCGATCTGCTCTACCAGGAGCTGCACGTGGACTCCGTGGACGCGCGCG	Db 985 GCCTGTGGGCCCCCATGCCTACTGCGGATCGGACATGAGAGGCCC OY 766 IGGTGCTTTATTAAAGTTACCAATGACAAGGTGAAAAGGTGAAAAGGTGAAAAGGTAAAGGTAAAAGGTAAAGGTAAAAGGTAAAGGTAAAAGGTAAAAGGTAAAAGGTAAAAGGTAAAAGGTAAAAAA	

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Sequence 590, Application US/10087192

Publication No. US2020182586A1

GENERAL INFORMATION:

APPLICANT: Brighland, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADACER.

FILE REFERENCE: 52946200122

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1302
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CORGANISM: Mus musculus
US-10-087-192-590
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SEQ ID NO 1612
LENGTH: 2036
                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Score 93.2; DB 13; Length Pred. No. 2.9e-19; 0; Mismatches 523; Indels

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212 583 272

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APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF UROKINASE PLASMINOGEN ACTIVATOR.
FILE REFERENCE: RTS-0188
FILE REPERENCE: RTS-0188
CURRENT APPLICATION NUMBER: US/10/665,216
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/821,972
PRIOR PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 168
SEQ ID NO 10
LENGTH: 2299
TYPE: DNA
ORGANISM: Mus musculus
FEATIFE:
                                                                                                                                                                                      Query Match
Best Local Similarity 49.7%;
Matches 586; Conservative
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; LOCATION: (59)...(1360)
US-10-665-216-10
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S-10-665-216-10
; Publication No. US20040043957A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
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AAB424	AAB42484 ID AAB42484 standard; protein; 560 AA.
X V	AAB42484;
X 담	08-FEB-2001 (first entry)
X 23 3	Human ORFX ORF2248 polypeptide sequence SEQ ID NO:4496.
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Æ.	latic; antiparkinsonian;
₹ 5	anticonvulsant, osteopathic, anticathritic, immunospipiessant, cardinated
₹ ₹	hypotensive; dermatological; immunosuppressive; antiinflammatory;
Κ¥	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
<u>₹</u>	antianaemic; gene therapy; cancer; proliferative disorder; nypertemblom;
3	neurodegenerative disorder; osteoarthritis; gratu vs most ursease, considering and disperse. Alsheres mellitus; hypothyroidism; SCID; AIDS;
3 3	Calulovaboular unbease, unables mortanes, affect, infection,
<u> </u>	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
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888	WPI; 2000-602362/57. N-PSDB; AAC76693.
X E E	ides derived from coers, proliferative
E	neurodegenerative disorders and cardiovascular disease.

AAO17144 standard; protein; 560

13-JUN-2002

AA017144;

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic, hepatotropic, vulnerary; squences have activities such as: cytostatic, hepatotropic, vulnerary; antiporvulant; antiparkinsonian; noctropic, natidiabetic; hypotensive; cardiant; thrombolytic; coapulant; vasorropic, antidiabetic; hypotensive; dermatological; immunosuppressant; immunostimulant; activities antidiabetic; antidiabetic; hypotensive; dermatological; immunosuppressive, antidialemency; antidiabetic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, disorders, osteoarthritis, graft vs host disease, cardiovascular disease, cororage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune catilage damage, nocturnal haemoglobinuria, antidiflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
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The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at mucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the human FSAP protein
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                                         Human, blood coagulation factor VII activating protease, FSAP, single-chain plasminogen activator; bleeding disorder, haematological,
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100.0%; Pred. No. 7.2e-181;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stoehr H, Feussner A,
Muth-Naumann G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 17-19; 27pp; German.
  coagulation factor
                                                                                                                                                                                                                                                                                                                                        26-JUL-2000; 2000DE-01036641.
10-0CT-2000; 2000DE-01050040.
21-0CT-2000; 2000DE-01052319.
12-APR-2001; 2001DE-01018706.
                                                                                                                                                                                                                                                                                          05-JUL-2001; 2001EP-00115691
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Best Local Similarity 100.
Matches 560; Conservative
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                                                                                                                                                                                              EP1182258-A1.
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roemisch J,
Nerlich C,
Human blood
                                                                                                 haemostatic.
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61 HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                        CGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AHCTDIKTRHLKVVLGDQDLKKEBFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHCTDIKTRHIKVVLGDODLKKEBFHEQSFRVQKIFKYSHYNBRDEIPHNDIALLKLKPV
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                                                                                                                                                                                                                                                       GEHN FCRN PDADEK PWCFIKVTNDKVKWBYCDVSACSAQDVAY PRESPTEPSTKL PGFDS
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                                                                                                                                  1 MFARMSDLHVLLLMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYBDYNQEBNTSSTLT
                                                                                                                                                                                                                                                                                                                      QFKGKFCEIGSDDCYVGDGYSYRGKMRTVNQHACLYWNSHLLLQENYNMFMEDAETHGI
                                                                                                                                                                           HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC
                                                                                                                                                                                                                                                                                                  181 QFKGKFCEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGI
                                                                                                                  1 MFARMSDIHVILILMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatocyte growth factor; protease; cleavage; active; inactive;
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                                                                                   Indels
                                                      99.7%; Score 3143; DB 5;
99.6%; Pred. No. 3.3e-180;
ive 1; Mismatches 1;
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sequence is the mutant human FSAP protein
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92JP-00312234
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(first entry)
                                                         Query Match
Best Local Similarity 99.6'
Matches 558; Conservative
                              Sequence 560 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
06-JAN-1995
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20-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                     CCKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA 360
                                                                                        AHCTDIKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPV 420
                                                                                                                AHCTDIKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPV 420
                                                                                                                                                                   DGHCALESKYVKTVCLPDGSFPSGSECHISGWGVTETGKGSRQLLDAKVKLIANTLCNSR 480
                                                                                                                                                                                                                                          540
                              CGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA 360
 GEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding mutant factor 7 activating protease, useful diagnosis, treatment and prevention of coagulation disorders, also related protein and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; blood coagulation factor VII activating protease; FSAP;
single-chain plasminogen activator; bleeding disorder; haematological;
haemostatic; mutant; mutein.
                                                                                                                                                                                                                             DGHCALESKYVKTVCLPDGSFPSGSECHISGWGVTBTGKGSRQLLDAKVKLIANTLCNSR
                                                                                                                                                                                                            QLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDGTYXVYGIVSWGLECGKRPGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         χ̈
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human blood coagulation factor VII activating protease mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 20-22; 27pp; German.
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Muth-Naumann G;
                                                                                                                                                                                                                                                                                                                                                                              AAO17145 standard; protein; 560
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10-OCT-2000; 2000DE-01050040.
21-OCT-2000; 2000DE-01052319.
12-APR-2001; 2001DE-01018706.
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N-PSDB; AAL45697.
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Synthetic.
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Nerlich C,
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AAO17145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                     Hepatocyte growth factor converting protease and precursor and gene
encoding them - for producing active two chain HGF from inactive single
chain HGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDIALLKLKPVDGHCALESKYVKTVCLPD--GSFPSGSECHISGWG-VTETGKG-SROLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACPDQFKGKFCEIGSDD-CYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA--ODVAYPEESPTEPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHPCWVLTAAHCTDIKTRH--LKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDEIPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPAALDPCASGPCLNGGSCSNTQDPQSYHCSCPRAFIGKDCGTEKCFDETRYEYLEGGD
                                                                                                                                                                                                                                                                                            Hepatocyte growth factor converting protease is capable of converting inactive single chain hepatocyte growth factor (HGF) into active two chain HGF by cleavage at a specific site. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DPCQPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKC--QKVQNTCK----D
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                                                                              Miyazawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                    26.4%; Score 833.5; DB 2; 33.6%; Pred. No. 6.5e-42; ive 89; Mismatches 220;
                                                                            Kitamura
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                                                                                                                                                                                                                                                        English.
                                                                            Morimoto
                                        CORP
                                                                                                                                                                                                                                                        Claim 12; Page 21-24; 30pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.6*
Matches 192; Conservative
                                      (MITU ) MITSUBISHI KASEI
                                                                      ж,
                                                                              Yamada
                                                                                                                  WPI; 1994-152921/19.
N-PSDB; AAQ63951.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 655 AA;
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셤 ò 임 ò ద standard; protein; 655

AAR89197

RESULT 5 AAR89197

AAR89197

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This is the amino acid sequence of the precursor protein of the inactive single chain form of a hepatocellular growth factor. The mature protein (AAR89196) has a mol. wt. of around 34 kD and is derived from the 96 kD precursor protein. The mature protein corresp. to residues 356-655 of the precursor protein. The inactive single chain form of the growth factor is activated by dimerisation of the mature protein. The active protein is a serine protease which can be used for the treatment of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMFMEDABTHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA--QDVAYPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPAALDPCASGPCLNGGSCSNTQDPQSYHCSCPRAFTG-----KD--CGTEKCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRSKFTCACPDOFKGKFCEIGSDD-CYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DPCOPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPCGRGQCL
                                   protein; inactive; single chain; hepatocellular growth factor; human; precursor; dimerisation; double chain; serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease
Human hepatocellular growth factor single chain precursor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.4%; Score 832.5; DB 2; Best Local Similarity 33.2%; Pred. No. 7.4e-42; Matches 192; Conservative 87; Mismatches 216;
                                                                                                                                                                 Location/Qualifiers
356. .655
/note= "mature pepti
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                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                       30-JAN-1996
                                                               liver; huma
hepatitis.
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10-APR-1991
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104 RDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPD--GSFPSGSECHISGWG-VTETGKG 460
                                                                       550 YSSSIREALVPLVADHKCSSPEVYGADISPNMLCAGYFDCK-SDACQGDSGGPLACEKNG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The modified t-PA has all/part of the kringle domains of native t-PA removed. The t-PA has functional properties superior to those of native tipA. It retains fibrin binding properties and interacts more slowly and inefficiently with plasminogen activator inhibitor(s) compared to native t-PA. It is obtd. in large anter. From a prokaryotic host. Modified to pis used for treating vascular disorders, eg deep vein thrombosis, pulmonary embolism, pertipheral arterial thrombosis, disseminated te-PA intravascular coaqulation, emboli from the heart or pertipheral arteries, associated with invasive cancers. t-PA is used at a dosage of 250000 to 5000000 units at a loading dose or in a deep vein thrombosis-pulmonary embolism, or 250000-7500000 units sor in a deep vein thrombosis-pulmonary infarction. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New modified tissue plasminogen activator - with new encoding DNA, new DNA expression vector, useful for treating vascular disorders, e.g., pulmonary embolism arterial thrombosis.
                -SROLLDAKVKLIANTLCNSROLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDG
                                                                                                                                                                                                                                                                                                                                     Tissue plasminogen activator; kringle domain; embolism; thrombosis; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 441;
                                                                                                                             609 VAYLYGIISWGDGCGRLHKPGVYTRVANYVDWINDRIR 646
                                                                                                             520 TYYVYGIVSWGLECGK--RPGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.8%; Score 812.5; DB 1; Best Local Similarity 37.7%; Pred. No. 8e-41; Matches 177; Conservative 70; Mismatches 163;
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                                                                                                                                                                                                                                                                                                               Modified tissue plasminogen activator.
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                                                                                                                                                                                                            AAP70643 standard, protein, 441
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N-PSDB; AAN70992.
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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10-APR-1991
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14;

Gaps

59;

Indels

ONTCKDNPCGRGOCLITOSPPYYR-----CVCKHPYTGPSCSQVVPV--CRPNPC 159

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The modified t-PA has all/part of the kringle domains of native t-PA removed. The t-PA has functional properties superior to those of native t-PA. It retains fibrin binding properties and interacts more alowly and inefficiently with plasminogen activator inhibitor(8) compared to native t-PA. Obtd. in large amts. from a prokaryotic host. Modified t-PA is used for treating vascular disorders, eg deep vein thrombosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508
                                                                                                                                                                                                                                                                                                            YSHYNERDEIPHNDIALLKIKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVT 455
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SHILLQENYNMFMEDAETHGIGEHNFCRNPDADEKFWCFIKVTNDKVKWEYCDVSACSAQ 279
                                                                                                                                                                                                                                                         280 DVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 SMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 SPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEBQKFEVBKYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETGKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; kringle domain; embolism; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGPLICEKDGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK
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pulmonary embolism arterial thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified tissue plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP70642 standard; protein; 473 AA.
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112 QNTCKDNPCGRGQCLITQSPPYYR -----CVCKHPYTGPSCSQVVPV--CRPNPC 159
                                                                                                                                                                                                                                                                                                            QNGATCSRHKRRSKFTCACPDQFKGKFCEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWN 219
                                                                                                                                                                                                                                                                                                                                                                              SHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                            280 DVAYPEESPIEPSIKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPGERFLCGGILISSCWILSAAHCFOERFPPHHLTVILGRTYRVVPGEEEOKFEVEKYIV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 YSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKEFD--DDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKH 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETGKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGD 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGD 423
                                                                                                                                                                                                                                                                           6
embolism, peripheral arterial thrombosis, disseminated intravascular coagulation, emboli from the heart or peripheral arteries, acute myocardial infarction, thrombotic strokes or fibrin deposits associated with invasive cancers. t-pA is used at a dosage of 250000 to 5000000 units at a loading dose or in a deep vein thrombosis-pulmonary embolism, or 250000-7500000 units over 30-90 mins. in acute myocardial infarction. (Updated on 25-WAR-2003 to correct pA field.)
                                                                                                                                                                                                                                                                       QVIČRĎE---KTÓMIYQČHQSWLRPVLRSNRVEYCWCN---SGRAQCHSVPVKSCSEPRC
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder.
                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGPLTCEKDGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                          DB 1; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel protein (useful for identifying genetic disorders) #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNWR
                                                                                                                                                                                                         Indels
                                                                                                                                                                      25.8%; Score 812.5; DB 1;
.larity 37.7%; Pred. No. 8.5e-41;
Conservative 70; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE07850 standard; protein; 689 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-2001; 2001US-0339739P.
11-DEC-2001; 2001US-0359453F.
14-MAR-2002; 2002US-035691P.
14-MAR-2002; 2002US-035334F.
12-APR-2002; 2002US-0372381P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                     Sequence 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003054152-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITQSPPYY-------RCVCKHPYTGPSCSQVV--PVCRPNPCQNGATCSRHK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 ATGTTVCACPPGFAGRLCNIEPDERCFLGNGTGYRGVASTSASGLSCLAWNSDLLYQELH 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 VDSVGAAALLGLGPHAYCRNPDNDERPWCYV-VKDSALSWEYCRLEACGPRRGQPGALMW 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------SAQDVAYPEESP----TEPSTKLPG-----FDSCGKTEIAER 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :|:||| ||: :||||| ||: :|||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                          Wang J;
Wang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DETRYBYLEGGDRWARVROGHVEQCEC - - - FGGRTWCEGTRHTACLSSPCLNGGTCHLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 RRSKFTCACPDOFKGKFCEIGSDD-CYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 KIK-RIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHCTDIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 -SVSVVLGQHFFNRTTDVTQTFGIEKYIPYTLYSVFNPSDH-DLVLIRLKKKKDDRCATRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 QALTEDGRPCRFPFRYGGRMLHACTSEGSAHRK---WCATTHNYDRDRAWGYCVBATPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHLKVVLGDQDLKKEEFFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDGTYYVYGIVSWGLECGK-~RPGVYTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ESLDPDWTPDQYDYSYEDYNQEBNTSSTLTHAENPDW-----YYTEDQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gabs
                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 119;
                                                                                                                                                                                                 Zhao OA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 689;
                                                                                                                                                                                          Zhang J, Zhao QA, yu P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSAC-
                                                                                                                                                              Ren F, Zuc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.6%; Score 807.5; DB 7; 31.3%; Pred. No. 2.4e-40; iive 89; Mismatches 213;
                                                                                                                                                                                                                         Weng G, Zi
Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 916; 1177pp; English
                                                                                                                                                                                             Goodrich RW,
                                                                                                                                                                                                                             Xue AJ, Wehrman T, W
g D, Chen R, Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 68
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-00128558.
24-APR-2002; 2002US-0376045P.
                                                                                                                                                                     Asundi V, Gooll.
A.T. Wehrman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                               2003-569235/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADE06939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 689 AA;
                                                                                                                                                                                                                                                             Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
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                                                                                                                                                                                                                                 Ghosh M,
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                                                                                                                                                                                             Tang
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KYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGV 454 271 VHKEFD--DDTYDNDIALLQLKSDSSRCAQESSVVRIVCLPPADLQLPDWTECELSGYGK 328 339 ISMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIF 396 219 NSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA The t-PA variants represented in AAR09215-63 (and the T252R or N184S analogues thereof or combinations thereof) and AAR09266-83 have their fibrinolytic activity turned off when generally in the plasma and activated when proximate to plasmin at the site of the clot thus providing specific localised clot therapy 160 ONGAŢCSRHKRRSKFŢCACPDQFKGKFCBIGS-DDCYVGDGYSYRGKMRTVNQHACLYW 279 QDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLT TETGKG--SROLLDAKVKLIANTLCNSROLYDHMIDDSMICAGNLOKPG-----ODTCOG 3 QVICRDE---KTQMIYQQHQSWLRPVLRSNRVEYCWCN---SGRAQCHSVPVKSCSEPRC 112 ONTCKDNPCGRGQCLITQSPPYR-----CVCKHPYTGPSCSOVVPV--CRPNPC DSGGPLTCEKDGTYYVYGIVSWGLBCGKR.-PGYYTQVTKFLNMIKATIK 555 Length 439; 25.4%; Score 802; DB 2; Length 43 37.7%; Pred. No. 3.4e-40; tive 68; Mismatches 165; Indels tissue plasminogen activator; infarction; coagulation. and delta(466-470) tPA variant. 1. 39 /label= Finger_domain Location/Qualifiers Ŗ. 92. .173 /label= Kringle_2 AAR13922 standard; protein; 434 90US-00486657 (revised)
(first entry) Query Match
Best Local Similarity 37.77
Matches 177; Conservative Sequence 439 AA; Delta(92-179) 01-MAR-1990; 09-JAN-2003 27-NOV-1991 05-SEP-1991 Synthetic 455 329 208 AAR13922 Key Domain Domain AAR1392 8 g 셤 કે g à 음 à 셤 ******** ò à g δ ů t-PA itissue plasminogen activator - activated only when proximate at site of clot and not systemically. F305H peen been peen peen mature been has been has d92-179, N184D, I210R, G211A, K212R, V213R, T252R, has /label= substitution /note= "F305 of the wild-type, mature t-PA has subtituted for H" t-PA has has has NF; Tissue plasminogen activator; zymogen; clot; plasma; plasmin 92-179 of the wild-type, /label= substitution /note= "V213 of the wild-type, mature t-PA subtituted for R" t-PA /label= substitution /note= "N184 of the wild-type, mature t-PA subtituted for D" /label= substitution /note= "1210 of the wild-type, mature t-PA subtituted for R" t-PA Paoni /label= substitution /note= "T252 of the wild-type, mature subtituted for R" mature mature Higgins DL, /label= substitution /note= "G211 of the wild-type, subtituted for A" /label= substitution /note= "K212 of the wild-type, subtituted for R" Botstein D, /note= "amino acids have been deleted" Location/Qualifiers 91. .92 Ā Claim 17; Page 44; 63pp; English 439 88US-00240856 89US-00384608 AAR09260 standard; protein; 668 VANYVDWINDQIR 680 (first entry) Anderson S, Bennett WE, 543 VTKFLNWIKATIK (GETH) GENENTECH INC WPI; 1990-115987/15. Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference 02-SEP-1988; 24-JUL-1989; t-PA variant Homo sapiens 409002798-A 22-MAR-1990 24-FEB-1993 Modified plasmin a AAR09260 Zoller

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                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                               This tPA variant has a deletion of amino acids Pro(466) to Leu(470) of the corresponding wild-type. The deletion is in the serine protease domain, making the variant more fibrin specific than the wild-type tPA. The variant also has a deletion of amino acids Cys(92) to Asp(179) of the wild-type sequence (1.e. Kringle I domain). See also AAR13917-R13921 and AAR14486. (Updated on 09-UAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 HEALSPFYSERLKEAHVRLYPSSRCTSQHLINRTVTDNMLCAGDTRSGGHDACQGDSGGP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 VHKEFD--DDIYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TETGKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGP 512
                                                                                                                                                                                                                                                                                                                          112 QNTCKDNPCGRGQCLITQSPPYYR.-----CVCKHPYTGPSCSQVVPV--CRPNPC 159
                                                                                                                                                                                                                                                                                                                                                                          QNGATCSRHKRRSKFTCACPDQFKGKFCEIGS-DDCYVGDGYSYRGKMNRTVNQHACLYW 218
                                                                                                                                                                                                                                                                                                                                                                                                57 FNGGTCOQALYFSDFVCQCPEGFAGKCCEIDTRATCYFGNGSAYRGTHSLTESGASCLPW 116
                                                                                                                                                                                                                                                                                                                                                                                                                         NSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 QDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 ISMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKBEFHEQSFRVEKIF 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEBQKFEVEKYI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 KYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGV 454
                                                                                          New tissue plasminogen activator variant used for vascular conditions - e.g. to prevent fibrin deposition of adhesion formation of reformation, deep vein thrombosis, peripheral vascular disease, embolism etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                        QVICRDE----KTOMIYQOHOSWLRPVLRSNRVEYCWCN---SGRAQCHSVPVKSCSEPRC
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          t-PA variant d92-179, I210R, G211A, K212R, V213R, T252R, F305H
                                                                                                                                                                                                                                                                         25.3%; Score 798.5; DB 2; Length 434; ilarity 37.6%; Pred. No. 5.4e-40; Conservative 70; Mismatches 165; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue plasminogen activator; zymogen; clot; plasma; plasmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNWR 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LICEKDGTYYVYGIVSWGLECGKR -- PGVYTQVTKFLNWIKATIK 555
                                                                                                                                          Claim 12; Page 27; 33pp; English
                                             Zoller ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR09261 standard; protein; 439
 90US-00486657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                      (GETH ) GENENTECH INC
                                             Gill JF, Presta LG,
                                                                     WPI; 1991-281468/38
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                      Seguence 434 AA;
 01-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-FEB-1993
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Matches 175;
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                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
                                           "amino acids 92-179 of the wild-type, mature t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proximate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The t-PA variants represented in AAR09215-63 (and the T252R or N184S analogues thereof or combinations thereof) and AAR09266-83 have their fibrinolytic activity turned off when generally in the plasma and activated when proximate to plasmin at the site of the clot thus providing specific localised clot therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 ONTCKDNPCGRGQCLITQSPPYR------CVCKHPYTGPSCSQVVPV--CRPNPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QVICRDE---KTQMIYQQHQSWLRPVLRSNRVEYCWCN---SGRAQCHSVPVKSCSEPRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 QNGATCSRHKRRSKFTCACPDQFKGKFCEIGS-DDCYVGDGYSYRGKMNRTVNQHACLYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= substitution
/note= "T252 of the wild-type, mature t-PA has been
subtituted for R"
                                                                                                                                                                                                    /label= substitution
/note= "G211 of the wild-type, mature t-PA has been
subtituted for A"
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/note= "F3305 of the wild-type, mature t-PA has
bublituted for H"
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                                                                                                                                                                                                                                                                                                                                                                                                        /note= "V213 of the wild-type, mature t-PA has subtituted for R"
                                                                                                                                                                                                                                                                                                                      t-PA has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paoni NF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
                                                                                                                                 mature t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                           mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified tissue plasminogen activator - activated plasmin at site of clot and not systemically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 797; DB 2; 37.4%; Pred. No. 6.7e-40;
                                                                                                                                                                                                                                                                                               /label= substitution
/note= "K212 of the wild-type,
subtituted for R"
                                                                                                          /label= substitution
/note= "I210 of the wild-type,
subtituted for R"
                                                                                                                                                                                                                                                                                                                                                                                             /label= substitution
Location/Qualifiers
                                                                  have been deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 44; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8BUS-00240856
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                      91. .92
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-115987/15.
                                                                                         Misc-difference 122
                                                                                                                                                                                  Misc-difference 123
                                                                                                                                                                                                                                                                           Misc-difference 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 439 AA;
Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zoller M;
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211 RSPGERHLGGGILISSCWILSAAHCEQERFPPHHLTVILGRTYRVVPGEESQKFEVEVEXI 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 VHKBFD--DDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGK 328
                                                                                                                                                                                                         NSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADERPWCFIKVTNDKVKWEYCDVSACSA
                                                                                                                                                                                                                                                                                      339 ISMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEBFHEQSFRVBKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYSHYNERDEI PHNDIALLKLKPVDGHCALESKYVKTVCLP.-DGSFPSGSECHISGWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETGKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQG
                                                                                                         112 ONTCKDNPCGRGQCLITQSPPYYR------CVCKHPYTGPSCSQVVPV--CRPNPC
                                                                                                                                                                                     160 QNGATCSRHKRRSKFTCACPDQFKGKFCEIGS-DDCYVGDGYSYRGKMNRTVNQHACLYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the wild-type, mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          has
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 has
                                                                      909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue plasminogen activator; zymogen; clot; plasma; plasmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSGGPLVCLNDGRMTLVGIISWGLGCGQXDVPGVYTKVTNYLDWIRDNMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSGGPLICEXDGTYYYYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     t-PA
                              Length 439;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= substitution
/note= "V213 of the wild-type, mature
subtituted for R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mature
                              25.2%; Score 795; DB 2; L. 37.4%; Pred. No. 8.8e-40; ive 70; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= substitution
/note= "I210 of the wild-type,
subtituted for R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= substitution
/note= "G211 of the wild-type,
subtituted for A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= substitution
/note= "K212 of the wild-type,
subtituted for R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91. .92
/note= "amino acids 92-179 of
have been deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K212R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G211A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein; 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1210R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                     Similarity 37.4% (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (1997) Since (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
Sequence 439 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                Query Match
Best Local Simi
Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
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                                                                                                                                                                                           KYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGV 454
                                                                                                                                                                                                                271 VHKEFD--DDTYDNDIALLIQLKSDSSRCAQESSVVRTYCLPPADLQLPDWTECELSGYGK 328
                                                                                                                                                                                                                                                                       507
                                                                                                                                                                                                                                                                                            329 HEALSPPYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQG 388
  NSMILRARRYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHV-LKNRRLRWEYCDVPSCS- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ů
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t-PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified tissue plasminogen activator - activated only when proximate plasmin at site of clot and not systemically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The t-PA variants represented in AAR09215-63 (and the T252R or N184S analogues thereof or combinations thereof) and AAR09266-83 have their fibrinolytic activity turned off when generally in the plasma and activated when proximate to plasmin at the site of the clot thus providing specific localised clot therapy
                                                                                                                                        RSPGERHLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYI
                                       QDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLT
                                                               339 ISMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEBFHEQSFRVEKIF
                                                                                                                                                                                                                                                                       TETGKG--SROLLDAKVKLIANTLCNSROLYDHMIDDSMICAGNLOKPG-----ODTCOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peen
                                                                                                                                                                                                                                                                                                                                                                    DSGGPLTCEKDGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabel= substitution
/note= "F305 of the wild-type, mature t-PA has
subtituted for H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ř,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue plasminogen activator; zymogen; clot; plasma; plasmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92-179 of the wild-type,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
91, 92
/note= "amino acids !
have been deleted"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR09258 standard; protein; 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88US-00240856
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89US-00384608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t-PA variant d92-179, F305H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-115987/15.
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Misc-difference
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24-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson S,
Zoller M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9002798-A
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623

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Ile(277)t-PA with extra finger- and extra growth factor-domains.
                                                                                             tissue plasminogen activator; finger domain; fibrinolysis
 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 623 AA;
                                                                                                                                                                                                                                                                                                                                                       (BEEC ) BEECHAM
                                                                                                                                                                                                                                                                                                         01-APR-1987;
                                                                                                                                                                                                                                                                                                                                  02-APR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         procedures.
                                                                                                                                                                                                                                                                                  14-0CT-1987
                                               07-JUN-1991
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                                                                                                                       Synthetic
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AAP71742
                         AAP71742;
                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONTCKDNPCGRGOCLITOSPPYYR------CVCKHPYTGPSCSOVVPV--CRPNPC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSPGERHLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :: |: |||||||:||
VHKEPD--DDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388
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                                                                                                                                                                                                                                                                                                                    The t-PA variants represented in AAR09215-63 (and the T252R or N184S analogues thereof or combinations thereof) and AAR09266-83 have their fibrinolytic activity turned off when generally in the plasma and activated when proximate to plasmin at the site of the clot thus providing specific localised clot therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISMPOGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETGKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNGATCSRHKRRSKFTCACPDQFKGKFCE1GS-DDCYVGDGYSYRGKWNRTVNQHACLYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSMILRARRYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHV-LKNRRLTWEYCDVPSCS-
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                         been
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                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                         t-PA has
                                                                                                                                                                                               NF.
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                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%; Score 794; DB 2; Length 439; 37.4%; Pred. No. 1e-39; tive 68; Mismatches 166; Indels
                                                                                                                                                                                                Paoni
           /label= substitution
/note= "F305 of the wild-type, mature
subtituted for H"
                                                                                                                                                                                               DĽ,
                                                                                                                                                                                             Higgins
                                                                                                                                                                                               Botstein D,
                                                                                                                                                                                                                                                                                             Claim 17; Page 44; 63pp; English
                                                                                                          88US-00240856
                                                                                                                                  88US-00240856
89US-00384608
                                                                                                                                                                                             Anderson S, Bennett WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                   WPI; 1990-115987/15.
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 176; Conserv
Misc-difference
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                                                                                                          02-SEP-1988;
                                                                                                                                  02-SEP-1988;
24-JUL-1989;
                                                           WO9002798-A
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                                                                                                                                                                                                        extra growth factor domain
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                                                                                                                  domain
                                                                                                                                                                                                                                                                 97. .623
/label= natural human tPA
/note= "Lys(277) replaced
                                                              9. .46
/label= extra finger
54. .87
/label= extra growth
location/Qualifiers
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Best Local Similarity 31.2
Matches 188; Conservative
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fibrinolytically active protease so that the catalytic site of the hybrid protein essential for fibrinolytic activity is optionally blocked by a removable blocking group. See also AAP71741-5
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                                                                                              ||||:::: | | :-|| | PWQAAIFAK--HRRSPGERFLCGGILISSCWILSAAHKFQERFPPHHLTVILGRTYRVVP
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                   VKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKH
                                      -----TCGLRQYSQPQF-RIIGGLFADIASH
                                                        PWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVJGDQDLKKE
                                                                                                                                       PSGSECHISGWGVTETGKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQK
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                                                                                               | :| | :| | :| | :| | CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATPGSYQVICRDE---KTQMI
                                                                                                                                                                                                                                                                                                        77 COPNECEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-----KVQNTCKDNPCGRGQCL
                                                                                                                                          ITQSPPYYR-----CVCKHPYTGPSCSQVVPV--CRPNPCQNGATCSRHKRRSKF
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                                                                                                                                                                                                                                        -----XSDDCYVGDGYSYRGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                   Indels 158;
   Length
'Match 25.1%; Score 792; DB 1; Lo
Local Similarity 31.2%; Pred. No. 1.9e-39;
Hes 188; Conservative 75; Mismatches 182;
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May 24, 2004, 09:43:55 ; Search time 16.5 Seconds (without alignments) 3264.682 Million cell updates/sec
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3154
1 MFARMSDLHVLJLLMALVGKT......TQVTKFLNWIKATIKSESGF 560
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                      OM protein - protein search, using sw model
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Perfect score:
Sequence:
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283366

283366 segs, 96191526 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	plasma hyaluronan-	plasma hyaluronan-	hepatocyte growth	coagulation factor	t-plasminogen acti	t-plasminogen acti	t-plasminogen acti	coagulation factor	ogen a	ogen	t-plasminogen acti	cto	act	act	u-plasminogen acti	u-plasminogen acti	u-plasminogen acti	act	ব	u-plasminogen acti	u-plasminogen acti	a	ω.	4	4	plasmin (EC 3.4.21	protein(a) (3.4	apolipoprotein(a)
	JC4795	JC5878	A46688	S28941	UKHUT	A35029	A29941	KFHU12	A34369	JS0598	JS0599	845281	JS0597	S18932	UKPG	JN0560	UKWS	UKBAY	PLBO	UKHU	A35005	JS0600	PLHU	B30848	PLPG	PLMS	800657	A61545	A32869
DB	: -	7	Н	~	Н	Н	Н	Н	Н	(1)	7	N	7	Н	Н	Н	٦	-	Н	Н	-	N	Н	N	Н	Н	Н	7	7
	560	558	655	603	562	559	S S S S	615	477	477	431	593	477	432	442	433	433	433	812	431	434	394	810	810	790	812	4548	455	1420
ery tch	: ;	80.2	26.4	4	24.3	4	m	m	m	m	N	ď	ď	ď	ij	21.7	ä	。	20.9	ö	。	ö	20.4	ö	ο,	ο.		œ.	•
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plasmin (EC 3,4.21 plasmin (EC 3,4.21	coagulation factor	macrophage-stimula	brain-specific ser	macrophage-stimula	hepatocyte growth	hepatocyte growth	hepatocyte growth	coagulation factor	macrophage-stimula	membrane-bound arg	thrombin (EC 3.4.2	thrombin (EC 3.4.2	coagulation factor	hepatocyte growth
146260 861545	EXCH	JC5061	JC5759	A40332	A60185	A35644	I51283	KFHU	A47136	JC7731	TBBO	TBHU	EXRT	JH0579
20	ı	Н	C)	Н	\vdash	Н	н	н	н	~	-	Н	~	Н
810	475	716	191	716	728	728	710	461	711	855	625	622	482	728
18.1	14.8	14.7	14.7	14.6	14.5	14.5	14.1	13.9	13.9	13.9	13.9	13.6	13.5	13.4
571.5	467.5	465	462.5	461	457.5	456.5	444	439.5	438.5	438.5	437.5	429	427	423.5
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 JC4795 plasma hy N;Alterna	RESULT 1 JC4795 plasma hyaluronan-binding protein precursor - human N;Alternate names: hepatocyte growth factor activator-like protein; PHBP
N;Contair C;Species C;Date: 1	/Contains: serine proteanase (EC 3.4.21) C;Species: Homo sapiens (man) C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
C, Accessi R, Choi -Mi	on: JC4795 ura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomita, M.
J. Blochem. A;Title: Pur	 Blochem. 119, 1157-1165, 1996 Brittle: Purification and characterization of a novel hyaluronan-binding protein (PHBP)
A, Referen	I activation: JC4795; MUID:96425001; PMID:8827452
A; Molecul	A;Accession: UC4/95 Monlecule type: mRNA Monci 1=50 / MUS
A; Cross-I	A,Cross-references: GB:583182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159
A, Experim A, Note: F	A/Experimental source: plasma A/Note: parts of this sequence, including the amino ends of the mature chains, were dete
C,Genetic	C;Genetics: A:Gene: GDB:HABP2; HABP; PHBP; HGPAL
A;Cross-1	A;Cross-references: GDB:4573962
C;Comples C;Superfa	: a disulfide-bonded heterodimer of chains produced from the same procursor; c mily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsi
C; Keyword	ls, chondroitin sulfate proteoglycan, glycoprotein, hyaluronic acid, nydrolase, main, signal segnance #status predicted <sig></sig>
F; 24-313/	Forduct: 25gram byalucnan-binding protein, 50K chain #status predicted <50K>
F;77-108, F;115-14	Domain: EGF homology <eg1> /Domain: EGF homology <eg2></eg2></eg1>
F;154-18	/Domain: EGF homology <eg3> //Domain: kringle homology <rr1></rr1></eg3>
F;314-55(F;314-516	//Domain: trypsin homology <try> //Product: plasma hyaluronan-binding protein, catalytic chain #status predicted</try>
F;54,207,	F;54,207/Binding site: carbohydrate (Asn) (covalent) #status predicted F;77-88,82-97,99-108,115-125,120-136,138-147,154-165,159-176,178-187,194-276,215-257,246
F;362,40	;,509/Active site: His, Asp, Ser #status predicted
Query Match Best Local Matches 56	Query Match Best Local Similarity 100.0%; Score 3154; DB 1; Length 560; Best Local Similarity 100.0%; Pred. No. 3e-188; Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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- q ₀	1
ζ	61 HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC 120
QQ	61 HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC 120
δλ	121 GRGQCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPD 180
QQ	121 GRGCCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPD 180

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Appendix to the factor activator (EC 3.4.21.-) precursor [validated] - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Species: Homo C; Homo C; Species: Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo C; Homo
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GEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDS
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R; Habhimoto, K.; Tobe, T.; Sumiya, U.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N.; Biol. Pharm. Bull. 20, 1127-1130, 1997

B; R; Habhimoto, K.; Tobe, T.; Sumiya, U.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N.; Biol. Pharm. Bull. 20, 1127-1130, 1997

B; R; Reference number: JC5878; MUD: 98065239; PMID: 9401717

A; Reference number: JC5878; MUD: 98065239; PMID: 9401717

A; Reference number: JC5878; MUD: 98065239; PMID: 9401717

A; Residues: 1-558 «HAS>

C; Comment: This protein acts as serine protein; EGF homology; kringle homology; trypsi

C; Superfamily: plasma hyaluronan-binding protein large chain #status predicted «MATL»

F; 1-23/Domain: EGF homology «EG2»

F; 113-145/Domain: EGF homology «EG3»

F; 113-145/Domain: EGF homology «KRI»

F; 113-28/Promain: kringle homology «KRI»

F; 112-28/Product: plasma hyaluronan-binding protein small chain #status predicted «MATE)

F; 112-185/Promain: trypsin homology «TRX»
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C;Species: Mus musculus (house mouse)
C;Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGQCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPD
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                                                                                                                                                                                                                                                                                                    AHCTDIKTRHLKVVLGDQDLKKSEFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGHCALESKYVKTVCLPDGSFPSGSECHISGWGVTETGKGSRQLLDAKVKLIANTLCNSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGHCALESKYVKTVCLPDGSFPSGSECHISGWGVTETGKGSRQLLDAKVKLIANTLCNSR
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                      QFKGKFCEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGI
                                                             QFKGKFCEIGSDDCYVGDGYSYRGKNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGI
                                                                                                                                        GEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDS
                                                                                                                                                                                            241 GEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDS
                                                                                                                                                                                                                                                         CGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA
                                                                                                                                                                                                                                                                                                                                                                                  361 AHCTDIKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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Best Local Similarity 78.5%
Matches 439; Conservative
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Qy 126 LITQSPPYY	QY 170 RRSKFTCACPDQFKGKFCEIGSD-DCYVGDGYSYRGKARRTVNQHACLYWNSHLLLQENY 228 191 VEGHHLCDCPMGYTGPFCDLDTTASCYEGRGVSYRGMARTTVSGAKCQRWASEATYR 247	Qy 229 NMFMEDAETHGIGEHNFCRNPDADEKFWCFIKVTNDKVKWEYCDVSACSAQDVAYPE- 285	QY 286ESPIEPSIK	OY 321 TAGKHPWQASLOSSLPLTISMPOGHPCGGALIHPCWVLTAAHCTDIKTRHLKVVLGDQ 378	Qy 379 DLKKEEFHEQSFRVEKIFKYSHYNERDEIPHNDIALLKI-KPVDGHCALESKYVK 432 Db 417 RHNQSCEHCQTLAVHSYRLHEAFSPSSYLNDLALLRLQKSADGSCAQLSPYVQ 469	QY 433 TVCLPDG-SPPSGSECHISGWGVTETGKGSRQLLDAKVKLIANTLCNSRQLYDHM 486	OY 487 IDDSMICAGNIQKPGODTCQGDSGGPLTCEKDGTYYVYGIVSWGLECGKRPGVYT 541	Qy 542 QVTKFLNWIK 551 Db 589 DVASYLTWIQ 598	RESULT 5 UVCHUT L-plasminogen activator (EC 3.4.21.68) precursor [validated] - human N,Alternate names: t-PA; tissue plasminogen activator C;Species: Homo sapiens (man) C;Date: 14.Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000 C;Date: 14.Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000 C;Date: 14.Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000 C;Date: 14.Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000 C;Date: 14.Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000 C;Date: The Structure of the human tissue-type plasminogen activator gene: A;Title: The structure of the human tissue-type plasminogen activator gene: A;Residues: 1.5c2 < NNT: A;Coss-references: GB:100141 A;Note: the codon given for residue 93 (ACC) is inconsistent with the author B; Pricarn Degen; A;Title: The human tissue plasminogen activator gene: A;Residues: 1.5c2 < NGC) A;Residues: 1.5c2 < DNA A;Residues: 1.5c2 < DNA A;Residues: 1.5c2 < DNA A;Residues: 1.5c2 < DNG A;Coss-references: GB:X03021; NID:g339817; PIDN:AAA98809.1; PID:g339818 R;Itagaki, Y; Y; Sadada #I; Moxinaga, T; Mitsuda, S; Higashio, R. A;Title: Purification and characterization of tissue plasminogen activator A;Title: Purification and characterization of tissue plasminogen activator A;Reference number: J70562; MUD:91291340; PMD:36881.1; PID:g441174 A;Residues: 1.5c2 < Lough A;Residues: 1.5c2 < Lough A;Reference number: J70562; MUD:91291340; PMD:360881.1; PID:g441174 A;Residues: 1.5c2 < Lough A;Residues: 1.5c2 < Lough A;Residues: 1.5c2 < Lough A;Reference number: J70562; MUD:91291340; PMD:360881.1; PMD:36081.1; PMD:370106.1066; PMD:270128; PMD:2706081.1; PMD:270106; PMD:270128; PMD:27060618 PMD:27010618 PMD:27010618 PMD:270128; PMD:27060618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 PMD:27010618 P	A; Note: part of this Sequence, including the amino con a part of A.; Ward, C.A.; Bennett R; Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett
OY 75DPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPCGRGQCL 126 DD 156 GGPAALDPCASGPCLNGGSCSNTQDPQSYHCSCPRAFTGKDCGTEKCF 203	Qy 127 ITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHK 169 Db 204 DETRYEVLEGGDRWARVRQGHVEQCECFGGRTWCEGTRHTACLSSPCLNGGTCHLIV 260	170	Qy 229 NMEMEDAETHGIGEHNFCRNPDADEKPWCPIKVTNDKVKWEYCDVSACSAQDVAXPEE 286 321 VDSVGADALLGLGPHAYCRNPDNDERPWCYV-VKDSALSWEYCRLEACESLTRVQLSPDL 379	OY 287 SPTEPSTKLPGFDSCGKTEIAERKIK-RIYGGFKSTAGKHPWOASLOSSLPLTISMPQGH 345	346 431	QY 404 RDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPDGSFPSGSECHISGWG-VTETGKG 460	QY 461 -SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDG 519	Oy 520 TYYVYGIVSWGLECCKRPGVYTQVTKFLNWIKATIK 555 : : : : : :	RESULT 4 S28941 N.Alternate names: Hageman factor C;Species: Cavia porcellus (guinea pig) N.Alternate names: Hageman factor C;Species: Cavia porcellus (guinea pig) C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000 C;Accession: 288941 R;Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.; Siemba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.; Biochim: Biochys. Acta 1159, 113-121, 1992 A;Attle: Primary structure of guinea-pig Hageman factor: sequence around the cleavage si A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:9900367; PMID:1390917 A;Reference number: \$28941; MUID:99003367; PMID:1390917 A;Reference number: \$28941; MUID:9900367; PMID:1390917 A;Reference number: \$28941; MUID:9900367; PMID:1390917 A;Reference number: \$28941; MUID:9900367; PMID:1390917 A;Reference number: \$28941; MUID:9900367; PMID:1390917 A;Reference number: \$28941; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:9900369; PMID:1390917 A;Reference number: \$289541; MUID:99000369; PMID:1390917 A;Reference number: \$289541; MUID:99000369; PMID:139000369; PMID:139000369; PM	87 C

Esche in CDNA A,Title: Cloning and expression of human tissue-type plasminogen activator A,Reference number: A93293; MUID:83115262; PMID:6337343 301, 214-221, 1983 e: Cloning and expr

A; Accession: A93293

A,Residues: 1562 <PEN>
A,Cross-references: GB:L00141
A,Cross-references: GB:L00141
A,Experimental source: melanoma cells
R,Sasaki, H,; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.
Nucleic Acids Res. 16, 5695, 1988
A,Title: Nuclectide sequence of the tissue-type plasminogen activator cDNA from human fe
A,Reference number: S02125
A,Reference number: S02125
A,Reference number: S02125
A,Reference number: S02125
A,Residues: 1-562 <ARS.
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A,Residues: 1-562 <ARS.
A,Reference number: A91343; MUID:85285620; PMID:3896853

human tissue plasminogen activ A/Accession: A91343
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Residues: 1-38, 'G', 86-433,'E', 435-562 <KAG>
A/Residues: 1-38, 'G', 86-433,'E', 435-562 <KAG>
A/Residues: 1-38, 'G', 86-433,'E', 445-562 <ARDIN G.; Holmgren, E.; Josephson,
B/Excitation of Consa aguences coding for a part of human tissue plasminoge
A/Reference number: A93951; MUD:83169656; PMID:6572897
A/Rocession: A93951
A/Residues: 251-358 <EDL>
A/Residues: 251-358 <EDL>

A; Experimental source: melanoma cells
R;Pohl, G:; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
Blochemistry 23, 3701-3707, 1984
A;Tille: Tissue plasminogen activator: peptide analyses confirm an indirectly derived differences.

A;References number: A90488; MUID:85000468; PMID:6433976
A;Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and R;Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and R;Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and R;Rebsolid G; Rablan, L.; Elmarsson, M.; Wallen, P.; Jornvall, H.
FEBS Lett. 168, 25-32, 1944
A;Reference number: A91322; MUID:84158956; PMID:6538514
A;Reference number: A91322; MUID:84158956; PMID:6538514
A;Reference number: A1320; PMID:84158956; PMID:6538514
A;Reference number: A1340; Userman, H.; Pannekoek, H.
J; Balo: Chem: Z61, 11414141424; Userman, H.; Pannekoek, H.
J; Balo: Chem: Z61, 1141414141, Pannekoek, H.
J; Reference number: A37567; MUID:87033611; PMID:302132
A;Contents: annotation; fibrin binding site
A;Reference number: A37568; MUID:87031612; PMID:303030
A;Contents: annotation; fibrin binding site
A;Reference number: A37568; MUID:87161; PMID:3142086
A;Contents: annotation; fibrin binding site
A;Reference number: A37568; MUID:89044681; PMID:3142086
A;Contents: annotation; fibrin binding site
A;Reference number: A60902; MUID:89044681; PMID:3142086
A;Contents: annotation; fibrin binding site
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A;Reference number: A50900401
A;Reference number: A50900401
A;Reference number: A509002
A;Reference number: A50900401
A;Reference number: A50900401
A;R

Residues: 1552 «HAR» Cross-references: GB:MISS18; NID:g190031; PIDN:AAA60111.1; PID:g190032 Note: parts of this sequence were confirmed by peptide sequencing Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C. A; Molecule type: n A; Residues: 1-562 A; Cross-references A; Note: parts of t R; Reddy, V.B.; Gaz

A, Reserence number: 190110; MOLD'SOCSTATO, FOLD'SOCSTATO, A, RESERVED NUMBER: 100110; MOLD'SOCSTATO, A, RESERVED NUMBER: 100110
A, ROCAGESTON: 160110
A, ROCAGESTON: 160110
A, ROCAGESTON: 160110
A, ROCAGESTON: 160110
A, RESIDENCE NUMBER: 1.56281, G; Thompson, D.; Tizard, R.; Schheuning, W.D.
A, RESIDENCE S. 1803-11230-11230, JBG;
A, RESIDENCE S. 1803-11230, JBG;
A, ACCESSION: 1650110
A, ACCESSION: 1650110
A, REFERENCE S. 1813-11230, JBG;
A, RESERVED NUMBER: 155232; MUID: 9528938; PMID: 3161893
A, RESERVED S. 1813-11230, JBG;
A, RESERVED S. 1813-1130, JBG;
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A, RESERVED S. 1813-1130, JBG;
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A, RESERVED S. 1813-1130, JBG;
A, RESERVED S. 1813-1130, JBG;
A, RESERVED S. 1813-1130, JBG;
A, RESERVED S. 1813-1130, J cells DNA 6, 461-472, 1987 A,Title: Expression of human uterine tissue-type plasminogen activator in mouse A,Reference number: 160110; MUID:88054470; PMID:2824147

ä

Length 562;

Gaps 85, COPNPCEHGGDC - - LVHGSTFTCSCLAPFSQNKCO-KVONTCKDNP--CGRG--Indels Query Match
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Best Local Similarity 35.0%; Pred. No. 2.6e-40;
Matches 182; Conservative 77; Mismatches 176; 77

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228 PDQFK-GKF-----CEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY 179 193 ò g

348 NMFMEDAETHG1GEHNFCRNPDADEKPWCF1KVTNDKVKWEYCDVSACSAQDVAYPEESP TEPSTKLPGFDSCGKTELAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG 250 229 셤 ò ઠે

343 406 401 349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDE GILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFD--DD 298 g ð

407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSPPSGSECHISGWGVTETGKG--SR 462

40 60 60 60 60 60 60 60 60 60 60 60 60 60	ABSULT 7 ACTIVATE A294LT 7 ACTIVATE A294LT 7 ACTIVATE TP 121.68) precursor - mouse C. Species: Mus musculus (house mouse) C. Species: Mus musculus (house mouse) C. Species: Mus musculus (house mouse) C. Species: 10-62p-1999 #sequence revision 10-8ep-1999 #text_change 10-8ep-1999 C. Accession: A29441, 848205, 548206 C. Accession: A29441, 848205, 1988 C. Accession: A29441, A29441, MUD: 88087303; PMID: 2826484 A. Reference number: A29941, MUD: 88087303; PMID: 2826484 A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 1-559 < RIC> A. Residues: 3-33-7, X, 39-40 < LIJ> A. Molecule type: protein A. Recession: S48205 A. Molecule type: protein A. Recession: S48207 A. Molecule type: protein A. Recession: S48207 A. Molecule type: protein A. Recession: S48207 A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein A. Molecule type: protein	A; Residues: 309-316 <li2> A; Residues: 309-316 <li2> A; Residues: 309-316 <lix> A; Residues: 33-37, X', 39-40 <liw> A; Residues: 33-37, X', 39-40 <liw> C; Superidues: 15 C; Superidues: 15 C; Superidues: 15 F; 10-17 / Domain: signal sequence #status predicted <sig> F; 10-17 / Domain: propeptide #status predicted <sig> F; 10-15 / Domain: propeptide #status predicted <ard> F; 10-15 / Domain: propeptide #status predicted <ard> F; 10-15 / Domain: propeptide #status predicted <ard> F; 10-15 / Domain: propeptide #status predicted <ard> F; 10-15 / Domain: propeptide #status predicted <ard> F; 10-15 / Domain: propeptide #status predicted <ard> F; 10-15 / Domain: propeptide homology <ard> F; 10-15 / Domain: propeptide homology <ard> F; 10-15 / Domain: propeptide homology <ard> F; 10-15 / Domain: propeptide homology <ard> F; 10-15 / Domain: propeptide homology <ard> F; 10-15 / Domain: propeptide homology <ard> F; 10-15 / Domain: propeptide #status predicted <bch> F; 10-15 / B; 10-16 / Domain: propeptide #status predicted <bch> F; 10-15 / B; 10-16 / Domain: propeptide #status predicted <bch> F; 10-15 / B; 10-16 / Domain: propeptide #status predicted <bch> F; 10-15 / B; 10-16 / Domain: propeptide #status predicted <bch> F; 10-15 / Domain: propeptide #status predicted <bch> F; 10-15 / Domain: propeptide #status predicted <bch> F; 10-15 / Domain: propeptide #status predicted <bch> F; 10-15 / Domain: propeptide #status predicted <bch> F; 10-15 / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: Propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status predicted / Domain: propeptide #status pred</bch></bch></bch></bch></bch></bch></bch></bch></bch></ard></ard></ard></ard></ard></ard></ard></ard></ard></ard></ard></ard></sig></sig></liw></liw></liw></liw></liw></liw></lix></li2></li2>
Db 402 TYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHBALSPPYSE 461 Cy 463 QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEK 517	DNA 7, 671-677, 1988 A,Title: Cloning and characterization of a CDNA for rat tissue-type plasminogen activa A,Title: Cloning and characterization of a CDNA for rat tissue-type plasminogen activa A,Reference number: A31597; MUD:89170114; PMID:3148445 A,Accession: A31597 A,Accession: A31597 A,Accession: A31597; MUD:89170114; PMID:3148445 A,Residues: 1-379, KK,381-559 «NYT> A,Residues: 1-379, KK,381-559 «NYT> A,Cross-references: GB:M23697; NID:g530159; PIDN:AA41812.1; PID:g530160 C,Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat h C,Reywords: fibrinollysis; glycoprotein; hydicolase; Kringle; serine proteinase F;1-17/Domain: signal sequence #status predicted <rig> F,10-59/Domain: signal sequence #status predicted <rig> F;30-59/Product: t-plasminogen activator fastus predicted <ach> F;30-59/Product: t-plasminogen activator chain A #status predicted <ach> F;30-59/Product: t-plasminogen activator chain B #status predicted <bch> F;213-294/Domain: kringle homology <kr2> F;213-259/Product: t-plasminogen activator chain B #status predicted <bch> F;30-559/Product: t-plasminogen activator chain B #status predicted F;30-559/Domain: trypsin homology <arn> F;30-559/Product: t-plasminogen activator chain B #status predicted F;30-558/Domain: trypsin homology <arn> F;30-559/Product: t-plasminogen activator chain B #status predicted F;30-558/Domain: trypsin homology <arn> F;30-559/Product: t-plasminogen activator chain B #status predicted F;30-558/Domain: trypsin homology <arn> F;30-559/Product: t-plasminogen activator chain B #status predicted F;30-289,297 F;30-59/F;00-30-306/F;00</arn></arn></arn></arn></bch></kr2></bch></ach></ach></rig></rig>	Query Match 24.0%; Score 757.5; DB 1; Length 559; Best Local Similarity 32.5%; Pred. No. 9.4e-40; 32.6%; Pred. No. 9.4e-40; Matches 202; Conservative 86; Mismatches 192; Indels 141; Gaps 29; QY 8 LHVLLLMALVGKTACG-FSLMSLLESLDPDWTPDQVDYSYEDYNQEBNTSS 57 Db 6 LCVLLLCGVAFTL

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A,Residues: 20-379 «MCM»
R;Fujiwaw, K., McMullen, B.A.
G. Biol. Chem. 258, 10924-10933, 1983
A,Title: Anino acid sequence of human beta-factor XIIa.
A,Reference number: A21037; MUID:83291041; PMID:6604055
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A; Residues: 1-615 <COO>
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A; Title: cDNA sequence coding for human coagulation factor XII (Hageman).
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A; Accession: A26814
A; Molecule type: mRNA
A; Residues: 4-615 <CRE:
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B; Col. Chem. 260, 13666-13676, 1988
A; Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the A; Reference number: A00930; MUD:86033830; PMID:3877053
A; Accession: A00930
A; Accession: A00930
A; Accession: A00930 g 2 coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human NyAlternate names: Hageman factor (activated) C)Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: To-Nov-1988 Hasequence_revision 30-Jun-1991 #text_change 08-Dec-2000 C;Accession: A29411; A26814; A0030; A25191; A22248; A21037 R;Cool, D.E.; MacGillivray, R.T.A. J.BST A21031 A2248; A21037 A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon A;Reference number: A29411; MUID:88007593; PMID:2888762 337 402 192 AGKYTTEFCSTPACP---KGK----SEDCYVGKGVTYRGTHSLTTSQASCLPWNSIVLM 243 EESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQG 344 FLCGGVLISSCWVLSAAHCFLERFPPNHLKVVLGRTYRVVPGBEEQTFEIEKYIVHEEFD 397 ERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPDGS--FPSGSECHISGWGVTETGKG 460 FFSDRLKEAHVRLYPSSRCTSQHLFNKTVTNNMLCAGDTRSGGNQDLHDACQGDSGGPLV 515 225 QENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYP 284 --DDTYDNDIALLQLRSQSKQCAQESSSVGTACLPDPNIQLPDWTECELSGYGKHEASSP --SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG----QDTCQGDSGGPLT 77 COPNPCEHGEDC - LVHGSTFTCSCLAPFSGNKCQ - KVQNTCKDNPCGRGQCLITQSPPY YRCVCKHPYTGPSC----SQVVPV----CRPNPCQ----NGATCSRHKRRSKFTC----ACPDQPKGKFCEIGSDDCYVGDGYSYRGKWNRTVNQHACLYWNSHLLL 345 HFCGGALIHPCWVLTAAHC--TDIKTRHLKVVLGDQDLKKEBFHEQSFRVEKIFKYSHYN A;Molecule type: mRNA A;Residues: 14-332, 'S',334-615 <CO2> A;Cross-references: GBM:11723; NID:g180358; PIDN:AAAS1986.1; PID:g180359 R:Que, B.G.; Davie, E.W. Biochemistry 25, 1525-1528, 1986 CMINKQMTLTGIISWGLGCGQKDVPGVYTKVTNYLDWIHDNMK 558 Best Local Similarity 35.0%; Pro Matches 183; Conservative 76; 134 285 338 456 83 296 403 461 515 쉼 à 셤 à DP δ g δ g ઠે g ò g ò g ò

A; Pathway: blood coagulation; fibrinolysis

C; Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology
C; Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology
C; Superfamily: coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma; if; 1.19/bomain: signal sequence #status predicted <SIG>
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F; 229-365/Region: proline-rich
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F; 3109/Binding site: carbohydrate (Thr) (covalent) #status experimental
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R;Mesiduces: 354-352,373-3615 <PUJ>
R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucese is present in the first epidermal growth factor domain of factor A;Reference number: A44606; MUID:92184750; PMID:1544894
A;Contents: annotation; carbohydrate binding site A; Gene: GDB:F12 A; Cross-references: GDB:119892; OMIM:234000 A; Map position: 5q34-5qter A; Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511. C; Complex: factor XII, prekallikrein, and HMW Kininogen form a complex bound to anionic ĭ Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma (Hageman factor) 34; 91 HGSTFTCSCLAPFSGNKCQKVQNTCKDNPCGRGQCL------ITQSPPYYRCVCKH 140 ----ADPC-QPNPCEHGGDCLV 90 A; Molecule type: mRNA A;Readidues: 146-378, 'G',380-615 <QUE> A;Cross-references: GB:M13147; NID:g180360; PIDN:AAA70224.1; PID:g180361 R;McMullen, B.A.; Fujikawa, K. J. Balol. Chem. 260, 5328-5341, 1985 A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa A;Reference number: A22248; MUID:85182674; PMID:3886654 113 MPSGPHCLCPQHLTGNHCQK-----EKCFEPQLLRFFHKNEIWYRTEQAAVARCQCKG Gaps e: Characterization of a cDNA coding for human factor XII rence number: A25191; MUID:86216049; PMID:3011063

```
t-plasminogen activator (BC 3.4.21.68) alpha-2 precursor - common vampire bat
N.Alternate names: tissue plasminogen activator
C.Species: Desmodus retundus (common vampire bat)
C.Species: Desmodus retundus (common vampire bat)
C.Accession: JS658
R.Kraetzschnar, J. Heandler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor
Gene 105, 229-27, 1991
A,Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A,Reference number: JS6597; MUID:92039036; PMID:1937019
A,Reference: GB:MG598; MUID:92039036; PMID:1937019
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A,Residues: 1-477 cKRAA
A,Residues: 1-477 cKRAA
A,Gross-references: GB:MG5988; NID:g166074; PIDN:AAA31593.1; PID:g166075
C.Superfamily: tissue plasminogen activator: EGF homology; fibronectin type I repeat hom
C; keywords: fibrinolygis; glycoprotein; hydrolase, kringle; serine proteinase
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F; 22-36/Domain: propeptide #status predicted cRAA
F; 22-36/Domain: kringle homology cRGF>
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F; 12-20/Domain: kringle homology cRGF>
F; 22-41/Domain: kringle homology cRGF>
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F; 22-226/Cleavage site: His-Ser (plasmin) #status predicted
F; 22-226/Cleavage site: His-Ser (plasmin) #status predicted
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AYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLOSSLPLTISM 341
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                                                                                                                                                                                                                                                                                           GKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQK----PG-QDTCQGDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- CVCKHPYTGPSCSQVVPV--CRPNPCQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 ATCSRHKRRSKFTCACPDQFKGKFCEIGSD-DCYVGDGYSYRGKMNRTVNQHACLYWNSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDV
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                                            :: |: :||||||:|| || || || :: ||||: :||||: :|||:|| :: || :|| :|| :|| :|| :|| :: || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
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23.2%; Score 731; DB 2; Length 47
Best Local Similarity 35.3%; Pred. No. 3.5e-38;
Matches 165; Conservative 74; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     GPLICEKDGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK
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                                                                                                POGHFCGGALIHPCWVLTAAHCTDIK-
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                                                         442
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSE-CHISGWGVTETGKGSRQ----LLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNL 497
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WCFV-LNRDRLSWEYCDLAQCQTPTQAAP---PTPVSPRLHVPLMPAQPAPPKPQPTTRT 331
                                                                                                                                                                                                                          ---GFDSCG-KTEIAERKIKRIYGGFKSTAGKHPWQASLQ 332
                                                                                                                                                                                                                                                                         332 PPQSQTPGALPAKREQPPSLTRNGPLSCGQRLRKSLSSMTRVVGGLVALRGAHPYLAALY 391
                                                                                                                                                                                                                                                                                                                          SSLPLTISMPQGH-FCGGALIHPCWVLTAAHCTDIK--TRHLKVVLGDQDLKK----EE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 SETTLCQVAGWG--HQFEGAEEYASFLQEAQVPFLSLERCSAPDVHGSSILPGMLCAGFL 552
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llarity 35.3%; Pred. No. 3.5e-38;
Conservative 73; Mismatches 171;
                                                                                                                            WCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPT-
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Best Local Similarity
Matches 165; Conserv
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A; Residues: 1-593 <SH1>
A; Residues: 1-593 <SH1>
A; Residues: 1-593 <SH1>
A; Residues: 1-593 <SH1>
A; Cross-references: GB: 20164
A; Cross-references: GB: 20164
A; Arcoss-references: GB: 20164
A; Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 2016
S; Pro, CRC for residue 203 as Phe, GTG for residue 247 as Leu, CRC for residue 286 as G is and Arc for residue 203 as Phe, GTG for residue 247 as Leu, CRC for residue 286 as G is and C for residue 203 as Val.
S; Fujikawa, K.; Walsh, K.A.; Davie, B.W.
Biochemistry 16, 2270-2278, 1977
A; Title: Isolation and characterization of bovine factor XII (Hageman factor).
A; Reference number: A61329; MUD: 77182112; PMID: 861210
A; Reference number: A61329; MUD: 77182112; PMID: 861210
A; Redidues: 10-16, X', 18-19; 525-550 <FUJ>
C; Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology C; Keywords: blood coagulation; fibrinolyais; glycoprotein; hydrolase; monomer; plasma; F; 122-160/Domain: Edf homology <EGF>
F; 122-160/Domain: Edf homology <ERP>
F; 122-160/Domain: trypsin homology <ERP>
F; 1230-287/Domain: trypsin homology <ERP>
F; 541/Active site: Ser #status predicted
                                                                                                                                                                                                                         Considerion factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
N.Alternate names: Hageman factor (activated)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S45281; A61329
R;Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys. Acta 1206, 63-70, 1994
A;Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comp. A;Reference number: S45281; MUID:94242782; PMID:8186251
A;Accession: S45281.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 - VCRINPCINGDSCLQAEGHR----LCRCAPSFAGRLCDVDLKASCYDDRDRGLSYRGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 AGTÍLSGAPÓSSWASBATY---WNVTABOVLNWGLGDHAFCRNPDNDTRPWCFI-WKGDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 GORLRKWLSSLNRVVGGLVALPGAHPYIAALYW------DOHFCAGSLIAPCWVLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHCTDIK--TRHLKVVLGDQDLKKBEFHEQS-------FRVEKIFK---YSHYNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AITPNPEKDQRWAYCLEPKKVKDHCSKANPCQKGGTCVNMPDGPRCICADHFIGKACQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 QNTCKDNPCGRGQCLITQSPPYYR---------CVCKHP--YTGPSCSQVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 SSTLTHAENPDWYY---TEDQADPC-QPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VINNMLCAGDIRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGEKDIPGV
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Pred. No. 1.4e-36;
                                                                                                        YTKVTNYLGWIRDNMR 430
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Best Local Similarity 33.0%;
Matches 191; Conservative 69
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A, Residues: 1-431 < KRAA
A, Residues: 1-431 < KRAA
A, Residues: 1-431 < KRAA
A, Residues: 1-431 < KRAA
A, Residues: 1-431 < KRAA
A, Coross-references: 1-431 < KRAA
A, Coross-references: 1-431 < KRAA
A, Coross-references: 10 Bus minogen activator; EGF homology; fibronectin type I repeat hom
C, Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C, Reywords: fibrinolysis; glyroprotein; hydrolase; kringle; serine proteinase
E, 22-36/Domain: bropeptide #status predicted < RGO
F, 37-441-M Product: plasminogen activator beta #status predicted < PLA>
F, 41-74/Domain: EGF homology < RGG>
F, 42-74/Domain: kringle homology < RGG>
F, 42-74/Domain: trypain homology < RGG>
F, 43-75/Domain: trypain homology < RGG>
F, 41-52, 46-63, 65-74, 82-163, 103-146, 134-158, 168-299, 211-227, 219-288, 313-388/Disulfide bon
F, 139, 352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F, 26-275, 382/Active site: His, Asp, Sex #status predicted
F, 345-361, 378-406/Disulfide bonds: #status predicted
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R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
Gene 105, 229-227, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat
A;Reference number: JS0597; MUID:92039036; PMID:1937019
A;Recession: JS0599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 VRAICLPEANLQLPDWTECELSGYGYGKSSPFYSEQLKEGHVRLYPSSRCTSKFLFNKT 354
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                                                                                                                                         510
                                                                                                                                                                        SSPFYSEQLKEGHVRLYPSSRCTSKFLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSG 429
                                      457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ST-GGLFTDITSHPWQAAIFAQ--NRRSSGERFLCGGILISSCWVLTAAHCFQERYPPQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 YRCVCKHPYIGPSCSQVVPVCRPNPCQNGAICSRHKRRSKFICACPDQFKGKFCEIGSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YROLARGSRAYGGCSEL-----RCFNGGTCWQAASFSDFVCQCPKGYTGKQCEVDTHA
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                                   HYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPDGS--FPSGSECHISGWGVTET
                                                                       Gaps
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                                                                                                                                                                                                                                            GPLICEKDGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK
                                                                                                                                                                                                                                                                           GPLVCMNDNHWILLGIISWGVGCGEKDIPGVYTKVTNYLGWIRDNWR
                                                                                                                                         GKG--SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.8%; Score 720.5; DB 2; 36.0%; Pred. No. 1.4e-37; iive 73; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 36.0°
Matches 157; Conservative
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Oy 526 IVSWGLECCKRPGVYTOVTKFLNWIK 551 Db 445 IISWGVGGEKDVPGVYTKVTNYLGWIR 472 *RESULT 14 \$18932 U-plasminogen activator (EC 3.4.21.73) precursor - rat N/Alternate names: plasminogen activator, urokinase-type; urinary plasminogen activator (5.5peciee: Rattus norvegicus (Norway rat) C.5peciee: 18-Oct-1989 #sequence revision 10-Feb-1995 #text_change 18-Jun-1999	Ryabbanitis S. S. Submitted to the submitted to the submitted to the submitted to the submitted to the submitted to the submitted to the submitted to the submitted to the submitted to the submitted to the submitted s	Db 198 LKNKGGSPPSFKCGGSLISPCWVASATHCFVNQPKKEETVVYLGQSKRNSINFGEMRFEV 25/
OY 405 DEIPHNDIALLKL-KPUDGHCALESKYVKTVCLPD-GSFPSGSECHISGWG-VTETG 458 1	RESULT 13 Subminicace nectivator (EC 3.4.21.69) alpha-1 precursor - common vamplie bat Subminicace names tissue plessingen activator (C. Dates 12.20) C. Dates and the subminication of the subminication of the vample bat C. Dates and the subminication of the subminication of the vample bat bat C. Dates and the subminication of the subminication of the vample bat bat R. Kratezachmar, J. J. Handler, B. J. Langer, G. J. Boidol, W.; Bringmann, P.; Alagon, A. J. Don Gene 105, 229-27, 1991 A. A. A. A. A. C. C. S. S. S. S. S. S. S. S. S. S. S. S. S.	385 LYPSSRCAPKFLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHWTLLG

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Search completed: May Job time: 17.5 secs
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F;152/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;179-310,220-236,228-299,324-393,356-372,383-411/Disnifide bonds: #status predicted
F;235,286,387/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                               GFG-QESATDYFYPKDLKMSVVKIISHEQCKQPHYKGSEINYKMLCAADPEWK-TDSCSG 375
                                       EKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPD--GSFPSGSECHIS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. Accession: A00932
R. Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 9525-9541, 1984
A.Title: cDNA and gene nucleotide sequence of porcine plasminogen activator.
A. Reference number: A00932; MUID:85087954; PMID:6096832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,Alternate names: uPA
;Species: Sus scrofa domestica (domestic pig)
;Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
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                                                                                                                                                                                                                                                                                                                                      DSGGPLTCEKDGTYYVYGIVSWGLECGK--RPGVYTQVTKFLNWIKATIKSESG 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Nagamine, Y.
submitted to the Protein Sequence Database, December 1986
A;Reference number: A37566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -plasminogen activator (EC 3.4.21.73) precursor - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contents: annotation; correction to residue 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i,Molecule type: DNA
1,Residues: 1-240,''', 242-442 <NAG1>
1,Residues: 1-240,''' , idney cell line LLC-PK1
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Matches 155; Conservative
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SwissProt_42:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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1D HGFA_MOUSE

AC GROSSS AA.

AC GROSSS & QSTAVA;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Hepatocyte growth factor activator precursor (BC 3.4.21.-) (HGF)

MATTER AND ACTIVATOR (HGFA).
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ilarity 34.4%; Pred. No. 4.4e-51;
Conservative 79; Mismatches 187; Indels 96; Gaps
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                                                                  SEQUENCE FROM N.A.

MEDLINE=21226753; PubMed=11032833;
van Adelsberg O.S., Sengal S., Kukes A., Brady C., Barasch J.,
van Adelsberg J.S., Sengal S., Kukes A., Brady C., Barasch J.,
Yang J., Huan Y.;
activation of hepatocyte growth factor (HGF) by endogenous HGF
activator is required for metanephric kidney morphogenesis in
vitro.";

J. Biol. Chem. 276:15099-15106(2001).

J. Biol. Chem. 276:15099-15106(2001).

J. Biol. Chem. 276:15099-15106(2001).

J. Biol. Chem. 276:15099-15106(2001).

J. Biol. Chem. 276:15099-15106(2001).

J. Sholling Advivates hepatocyte growth factor (HGF) by converting
thermal single chain on a heterodimeric form (By similarity).

J. SUBCELULIAR LOCATION: Secreted as an inactive single-chain
precursor and is then activated to a heterodimeric form (By similarity).

J. SIMILARITY: Contains 1 fibronectin type II domain.

J. SIMILARITY: Contains 1 fibronectin type II domain.

J. SIMILARITY: Contains 1 kringle domain.
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RE MENE, AF090171, AAF03418.1; -

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  "Mouse hepatocyte growth factor activator.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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239 203 263 351 404

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IPR001254; Peptidase_S1.
IPR001314; Peptidase_S1A.
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TESUZELLIVET;

MEDLINE=39003367; PubMed=1390917;

MEDLINE=39003367; PubMed=1390917.

A Rambara T., Okabe H.;

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                                                                                                                                                            632
                            430 YVKTVCLPD--GSFPSGSECHISGWGVTE--TGKGSRQLLDAKVKLIANTLCNSRQLYDH 485
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514 FVQPICLPEAGSSFPTGHKCQIAGMGHMDENVSSYSNSLLEALVPLVADHKCSSPEVYGA
                                                                                                                                         486 MIDDSMICAGNLOKPGODICQGDSGGPLICEKDGIYYVYGIVSWGLECGK--RPGVYTQV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavlidae; Cavia.
MCBI_TaxID=10141;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Coaquiation factor XII precursor (EC 3.4.21.38) (Hageman factor)
(HAP) (Fragment).
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InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF InterPro; IPR000083; Fibrnctnl.
InterPro; IPR000652; Fibrnctnl.
InterPro; IPR000652; Fibrnctnl.
InterPro; IPR006210; IEGF.
InterPro; IPR000011; Kringle.
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633 ANYVDWINDRIR 644
                                                                                                                                                                                                         544 TKFLNWIKATIK 555
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MEROPS; S01.211;
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DR SWART; SMOOD20; Tryp SPc; 1.

DR PROSITE; PSO1022; EGF 1; 2.

DR PROSITE; PSO1022; EGF 2; 1.

DR PROSITE; PSO1023; FIBRONECTIN 1; 1.

DR PROSITE; PSO0023; FIBRONECTIN 2; 1.

DR PROSITE; PSO0021; KRINGLE 2; 1.

DR PROSITE; PSO0021; KRINGLE 2; 1.

DR PROSITE; PSO0124; TRYPSIN DOM; 1.

DR PROSITE; PSO135; TRYPSIN DOM; 1.

DR PROSITE; PSO135; TRYPSIN SER; 1.

RECORD STATE STORE STORE STORE STORE STORE SER; 1.

THE PROSITE; PSO0135; TRYPSIN SER; 1.

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ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
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FIBRONECTIN TYPE-I.
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KRINGLE.
PEam; PP00039; En1; 1.
PEam; PP00040; En2; 1.
PFam; PP00051; kringle; 1.
Pfam; PP00051; kringle; 1.
PFANTS; PR00722; CHYMOPRYESIN.
PRINTS; PR0013; PNTYPEII.
PRINTS; PR0013; PNTYPEII.
PRINTS; PR00198; KRINGLE.
PRODOM; PD000995; RI TYPE-II; 1.
SWART; SW00181; EGP; 2.
SWART; SW00181; EGP; 2.
SWART; SW00189; RN1; 1.
SWART; SW00180; RN1; 1.
SWART; SW00180; RN1; 1.
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Nucleic Acids Res. 16:5695-5695(1988)

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                                                                                                                                                                                                                                                                                                                                                                                366 LPGAHPYIAALYWG-----SNPCSGSLIAPCWVLTAAHCLQNRPAPEELKVVLGQD 416
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                   CLEPKKVKDHCSKHNPCQRGGICVNTLSSPHCLCPDHLTGKHCQ------REKC
                                                                                                                                                               191 VEGHHLCDCPMGYTGPFCDLDTTASCYEGRGVSYRGMARTTVSGAKCQRWASEATYR---
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                                                                   -- RCVCKHPYTGPSCSQV-VPVCRPNPCQNGATCSRHK
                                                                                                     135 FEPÓLHRFFHENEIWFRIGPAGVAKCHCKGP--DAHCKOMHSQECQTNPCLNGGRCL--E
                                                                                                                                      170 RRSKFTCACPDQFKGKFCEIGSD-DCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                                                                                                    --ESPTEPSTK-----KIKRIYGGFKS
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MEDLINE=83115262; PubMed=6337343;
MEDLINE=8115262; PubMed=6337343;
MEDLINE=8115262; PubMed=6337343;
Mard C.A., Bennett W.F., Yelverton B., Seeburg P.H., Heyneker H.L., Goeddel D.V., Collen D.;
"Cloning and expression of human tissue-type plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fetal lung;
MISTINESES626279.PubMed=3133640;
SasaXi H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
SasaXi H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
"Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fetal lung cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P00750, Q1510.7
21-UTL-1986 (Rel. 01, Last sequence update)
21-UUL-1986 (Rel. 01, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
15-WAR-2rype plasminogen activator precursor (BC 3.4.21.68) (tPA)
1c-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
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Nature 301:214-221(1983).
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                                                                   LITQSPPYY-
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MEDLINE=22388257; PubMed=12477932;

Astrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rokarstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
                                                                      Wei C.-M., Watkins P., Galli J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Umbilical vein;
MEDINE-201219; PubMed=2107528;
Siebbert P.D., Fong K.;
"Variant tissue-type plasminogen activator (FLAT) cDNA obtained from
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=84291137; PubMed=6089198;
MPDLINE=84291137; PubMed=6089198;
MPT., Elgh F., Lund B.;
"The structure of the human tissue-type plasminogen activator gene: correlation of intron and exon structures to functional and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILIRE=86284200; PubMed=3090401;
MEDILIRE=86284200; PubMed=3090401;
MEDILIRE=86284200; PubMed=3090401;
Opdenaker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
Cloning of cDNA coding for human tissue-type plasminogen activator and its expression in Escherichia coli.";
Moi. Biol. Med. 3:279-292(1986).
                                                                                          "Expression of human uterine tissue-type plasminogen activator in mouse cells using BPV vectors.";
DNA 6:461-472(1987).
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MEDLINE-83169656; PubMed-6572897;
Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
Josephson S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences coding for a part of human tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                     structural domains.";
Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
                                                                                                                                                                                                   MEDLINE-86196143; PubMed=3009482; Friezner Degen S.J., Rajput B., Reich E.; "The human tissue plasminogen activator gene."; J. Biol. Chem. 261:6972-6985(1986).
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Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983)
                                                   LINE=88054470; FubMed=2824147;
Idy V.B., Garramone A.J., Sasak H.,
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Nucleic Acids Res. 18:1086-1086(1990)
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SEQUENCE FROM N.A.
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SEQUENCE OF 1-36
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                                                                                        Hsiung N.;
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SEQUENCE OF 36-562.
TISSUE-Melanoma;
MEDLINE-85000468; PubMed-6433976;
MEDLINE-85000468; PubMed-6433976;
Milson G., Kaelletroem M., Bergadorf N., Wallen P., Joernvall H.;
Wissue plasminogen activator: peptide analyses confirm an indirectly derived anino acid sequence, identify the active site serine residue, establish glycosylation sites, and localize variant differences.";
Biochemistry 23:3701-3707(1984). [11]
SEQUENCE OF 31-562 FROM N.A.
MEDIINE-91291340; PubMed-1368681;
Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
"Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
Agric. Biol. Chem. 55:1225-1232(1991). MEDLINE-85289338; PubMed=3161893; Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R., Schleuning W.-D.; "Isolation and characterization of the human tissue-type plasminogen activator structural gene including its 5' flanking region."; J. Biol. Chem. 260:11223-11230(1985). X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
MEDLINE=96200985; PubMed=8613982;
Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
Bode W.;
"The 2.3 A crystal structure of the catalytic domain of recombinant
two-chain human tissue-type plasminogen activator.";
J. Mol. Biol. 258:117-135(1996). MEDLINE=97449126; PubMed=9305622; Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert Bode W.; X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2. MEDLINE=92118803; PubMed=1310033; MEDLINE=92118803; PubMed=1310033; Med Vos A., Ultsch M.H., Kalley R.F., Padmanabhan K., Tulinskly A., Westbrook M.L., Kossiakof A., "Crystal structure of the kringle 2 domain of tissue plasminogen TISSUE=Melanoma; MEDLINE=83209620; PubMed=6682760; Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.; "Purification and characterization of a melanoma cell plasminogen MEDLINE-91244765; PubMed-1645336; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.; Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.; "Disulfide pairing of the recombinant kringle-2 domain of tissue plasminogen activator produced in Escherichia coli."; J. Biol. Chem. 266:10070-10072(1991). Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.; "Tissue plasminogen activator has an O-linked fucose attached threonine-61 in the epidermal growth factor domain."; Biochemistry 30:2311-2314(1991). MEDIINE=90092112; PubMed=2513186; Pfelffer G., Schmidt M., Strube K.-H., Geyer R.; "Carbobydrate structure of recombinant human uterine tissue plasminogen activator expressed in mouse epithelial cells."; Eur. J. Blochem. 186:273-286(1989). X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN "Lysine 156 promotes the anomalous proenzyme activity crystal structure of single-chain human tPA."; EMBO J. 16:4797-4805(1997). Eur. J. Biochem. 132:681-686(1983) CARBOHYDRATE-LINKAGE SITE THR-96. MEDLINE=91159408; PubMed=1900431; SEQUENCE OF 33-52 AND 311-330. STRUCTURE OF CARBOHYDRATES DISULFIDE BONDS IN KRINGLE activator."; 18]

-QCLIIQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178 QLIDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTCEK 517 146 AECTNWNS----SALAQKPYSGR------RPDAIRLGLGNHNYCRNPDRDSKPWCYV 192 TEPSTKLPGFDSCGKTE1AERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP 298 -----TCGLRQYSQPQF-RIKGGLFADIASHPWQAAIFAK--HRRSPGERFLCG 349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNBRDE 407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR COPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP--CGRG-----STRUCTURE BY NMR OF KRINGLE 2.
MEDLINE=90122799; PubMed=2558718;
Byeon I.-J.,, Kelley R.F., Llinas M.;
"IH NMR structural tracterization of a recombinant kringle 2 domain
"IH nms structural characterization of a secombinant kringle 2 domain
"IF om human tissue-type plasminogen activator.";
Biochemistry 28:9350-9360(1989). PDQFK-GKF-----CEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY STRUCTURE BY NMR OF KRINGLE 2.
MEDLINE-92106329; PubMed-1762144;
Bycon I.--U., Llinas M.;
Bycon structure of the tissue-type plasminogen activator kringle
"Solution structure of the tissue-type plasminogen activator kringle
g domain complexed to 6-aminohexanoic acid an antifibrinolytic STRUCTURE BY NMR OF KRINGLE 2.
MEDLINE-91200042; PubMed=1901789;
Byeon I.-J.L., Kelley R.F., Llinas M.;
"Kringle-2 domain of the tissue-tyse plasminogen activator. IH-NMR assignments and secondary structure.";
Eur. J. Biochem. 197:155-165(1991). 85; Length Indels Query Match
24.3%; Score 766.5; DB 1;
Best Local Similarity 35.0%; Pred. No. 9.4e-47;
Matches 182; Conservative 77; Mismatches 176; Ą update) Created) Last sequence PRT; drug."; J. Mol. Biol. 222:1035-1051(1991). 2.4-A resolution."; 31:270-279(1992). STANDARD; (Rel. 17, (Rel. 20, 1 TPA RAT P19637; 01-FEB-1991 01-NOV-1991 activator at Biochemistry 518 463 17 98 179 193 229 250 RESULT S SEA g à g g g ð g ò ઠ ò d ò В ઠે 요 $\dot{\delta}$ ò ţ ō

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Gaps

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REQUENCE FROM N.A.

**REGISTANCE FROM N.A.

**REGISTANCE OF THE TATA-less rat tissue-type plasminogen activator

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PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY FLASMIN, TISSUE XALLIKREIN OF FACTOR XA.

MISCELLANEOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity. SIMILARITY: Belongs to peptidase family SI.

SIMILARITY: Contains I EGF-like domain.

SIMILARITY: Contains I fibronectin type I domain.
                                                                                                                        Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
  10-OCT-2003 (Rel. 42, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
(t-PA) (t-plasminogen activator).
                                                                                                                                                                                                                                                      MEDLINE-89170114; PubMed~3148445;
Ny T., Leonardsson G., Hsueh A.J.W.;
"Cloning and characterization of a cDNA for rat tissue-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, M23697, AAA41812.1;
EMBL, M31897, AAA42261.1;
EMBL, M311897, AAA42261.1;
EMBL, M31188, AAA42261.1;
EMBL, M31188, AAA42261.1;
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EMBL, M31196, AAA42261.1;
EMBL, M31196, AAA42261.1;
EMBL, M31196, AAA42261.1;
EMBL, M31196, AAA4261.1;
EMBL, M31196, AAA4261.1;
EMBL, M31196, AAA4261.1;
EMBL, 
                                                                                                                                                                                                                                                                                                                              plasminogen activator.";
DNA 7:671-677(1988).
                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI TaxID=10116;
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TISSUE-TYPE PLASMINOGEN ACTIVATOR. TISSUE-TYPE PLASMINOGEN ACTIVATOR A CHAIN. TISSUE-TYPE PLASMINOGEN ACTIVATOR B

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--TYQQHQSWLRPMLRGNRVEYCRCNSGLAQCHSVPVRSCSEPRCFNGGTCQQALYFSDF 103
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InterPro; IPR009003; Cys_Ser_trypsin. InterPro; IPR006209; EGF like. InterPro; IPR006083; Fibrnchl. InterPro; IPR006210; IEGF.

P00750; 1RTF

HSSP;

MEROPS; S01.232;

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PKGPTEDCYVGKGVTYRGTHSFTTSKASCLPWNSMILIGKTYTAWRANSQALGLGRHNYC 265
                                                                                                                                                                                                                                                                             360 RFPPHHLKVVLGRIYRVVPGEEEQTFEIEKYIVHKEFD--DDIYDNDIALLQLRSDSSQC 417
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                       VCQCPDGFVGKRCDIDTRATCFE---GQG---IT-----YRGTWSTAENGAECINWNSSA 152
                                                                                --SQVVPVCRPNPCQNGATCSRHKRRSKFTCACPDQ------FK-GKF-----C 187
                                                                                                                         153 LSOKPYSARRPNAIKLG--LGNHN----YCRNPDRDVKPWCYVFKAGKYTTEFGSTPAC 205
                                                                                                                                                                 EIG-SDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGIGEHNFC 246
                                                                                                                                                                                                                                                   RNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDSCGKTEI 306
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                                                                                                                                                                                                                                                                                                                                                                             303 KOPOF-RIKGGLFIDITSHPWQAAI--FVKNKRSPGERFLCGGVLISSCWVLSAAHCFVE 359
                                                                                                                                                                                                                                                                                                                                                                                                                       365 DIKTRHLKVVLGDQDLKKBEFHEQSFRVEKIFKYSHYNBRDEIPHNDIALLKLKPVDGHC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 QLYDHMIDDSMICAGNLQKPG----QDTCQGDSGGPLTCEKDGTYYVYGIVSWGLECGKR 536
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TISSUE=Mammary gland;
MEDIATE=2388257; PubMed=12477932;
Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuvik S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Rickles R.J., Dubmed=2826484;

Rickles R.J., Darrow A.L., Strickland S.;

Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcinoma cell Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. TPA_MOUSE STANDARD, PRT, 559 AA.
P11214; Q91VP2;
01-JUL-1989 (Rell. 11, Created)
10-CCT-2003 (Rell. 42, Last sequence update)
15-MAR-2004 (Rell. 43, Last annotation update)
Tissue-type plasminogen activator precursor (BC 3.4.21.68) (tPA) (t-PA) (t-plasminogen activator). differentiation.";
J. Biol. Chem. 263:1563-1569(1988). Mus musculus (Mouse) SEQUENCE FROM N.A. NCBI_TaxID=10090;

Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;

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RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", 99:16899-16903(2002).

P. C. I. FUNCTION: Converts the abundant, but inactive, zymogen plasminogen. Controlling plasmin-mediated proteolysis, it plays an important controlling plasmin-mediated proteolysis, it plays an important controlling plasminogen and degradation, in cell migration and many other physiopathological events.

C.!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin A and chain B held by a disulfide bond. -:- SUBCELLULAR LOCATION: Secreted, extracellular.
-:- PTH: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENSTWE, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-:- MISCELLANDEDUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
-:- SIMILARITY: Conteains 1 EGF-like domain.
-:- SIMILARITY: Conteains 1 EdF-like domain.
-:- SIMILARITY: Conteains 2 kringle domains. EMBL; J03520; AAA40470.1; -.

DD 452 ASSPFFSDRLKEAHVRLYPSSRCTSQHLFNKTVTNNMLCAGDTRSGGNQDLHDACQGDSG 511 QY 511 GPLYCERDGTXYVYGIVSWGLECGKRPGVYTQVTKPLNWIKATIK 555	ULT 7 2 HUMAN FRA12 HUMAN ST P00748; P78339;			RY SEQUENCE FROM N.A. RX MEDINE=88007593; PubMed=2888762; RX COOl D.E., McGillivay R.T.A.; RT "Characterization of the human blood coagulation factor XII gene. RT Intron/exon gene organization and analysis of the 5'-flanking RT region."; RT region.";	[2] SEQUENCE Rieder M. Rajkumar Submitted			MEDLINE-86033830; PubMed-3877053; Cool D.E., Edgell CJ.S., Louie G.V., MCGillivray R.T.A.;	"Characterization or muman blood coequiation factor All Prediction of the primary structure of factor XII and th structure of beta-factor XIIa."; J. Biol. Chem. 260:13666-13676(1985).		Eattor)."; Biochemistry 25:1525-1528(1986). [6]			RA MEDIATURE STATUS, FUNCTULIBER B.A.; RA FUJIKAWA K., McMullen B.A.; RT "Amino acid sequence of human beta-factor XIIa."; RI J. Biol. Chem. 258:10924-10933(1983).	
KW Plasma; Kringle; EGF-like domain; Repeat; Signal. FT SIGNAL 1 17 FT PROPEP 18 29 FT CHAIN 30 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR. FT CHAIN 30 308 TISSUE-TYPE PLASMINOGEN ACTIVATOR A	CHAIN 309 559 TISSUE-1. DOMAIN 36 78 FIBRONEC DOMAIN 124 205 KRINGLE	DOMAIN 213 294 DOMAIN 309 559 ACT SITE 404 ACT SITE 510 510	DISULFID 38 68 BY SIMILARITY DISULFID 66 75 BY SIMILARITY DISULFID 83 94 BY SIMILARITY DISULFID 88 105 BY SIMILARITY DISULFID 107 116 BY SIMILARITY DISULFI	DISOLETED 124 205 BY DISOLETED 145 205 BY DISOLETED 176 200 BY DISOLETED 234 276 BY DISOLETED 254 276 BY DISOLETED 257 428 IN	DISULFID 340 356 DISULFID 348 417 DISULFID 442 516 DISULFID 474 490 DISULFID 506 534 CARROCHYD 149 149	COMPLICT 260 260 G -A (IN REF. 1). CONFLICT 325 325 P -A (IN REF. 1). SEQUENCE 559 AA; 63122 MW; 8CCEEZBDB94514D9 CRC6	Query Match Best Local Similarity 35.1%; Pred. No. 7.7e-46; Matches 185; Conservative 75; Mismatches 168; Indels 99; Gaps 22;	QY 77 CQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNPCGRGQCLITQSPPY 133	QY 134 YRCVCKHPYTGESCSQVVPVCRENPCQNGATCSRHKRRSKFTC 176	Qy 177ACPDQFKGKFCEIGSDDCYVQDGYSYRGXMNRTVNQHACLYWNSHLLL 224	Qy 225 GENYNMFWEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYP 284 ::	OY 285 EESPTEPSTKLPGFDSCGKTEIABRKIKRIYGGFKSTAGKHPWQASLQSSLPLTIS 340	OY 341 MPQGHFCGGALIHPCWVLTAAHCTDIKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKY 398 334 PGERFLCGGVLISSCWVLSAAHCFLERFPPNHLKVVLGRTYRVVPGEEEQTFEIEKYIVH 393	QY 399 SHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPDGSFPSGSECHISGWGVTE 456 ::	OY 457 TGKGSRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSG 510

Engel W.; factor

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MEDLINE=96133302; PubMed=8528215; Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Enge. Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Enge. "The novel acceptor splice site mutation 11396 (G-->A) in the fact. XII gene causes a truncated transcript in cross-reacting material negative patients."; Hum. Mol. Genet. 4:1235-1237(1995).
                                                                          CARBOHYDRATE-LINKAGE SITE THR-109.
MEDLINES-92184750; PubMed=1548894;
Harris R.J., Ling V.T., Spellman M.W.;
Harris R.J., Ling V.T., Spellman M.W.;
Tolinked fuccose is present in the first epidermal growth factor
domain of factor XII but not protein C.";
J. Biol. Chem. 267:5102-5107(1992).
                                                                                                                                                VARIANT WASHINGTON D.C. SER-590.
MEDLINE-90046788; PubMed=2510163;
Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving
Saito H.;
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EMBL; AF538691; AAM97932.1; --
EMBL; M1723; AAA51986.1; --
EMBL; M1746; AAB59490.1; --
EMBL; M1746; AAB59490.1; JOINED.
EMBL; M13147; AAA59490.1; JOINED.
EMBL; M13147; AAA59490.1; --
EMBL; W1746; AAA59490.1; --
EMBL; W1746; AAA59490.1; --
EMBL; W17474; AAA59490.1; --
EMBL; W71274; AAA594.1; --
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Conservative
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Matches
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MEDINE-9290785; PubMed=10361128;
MEDINE-9290785; PubMed=10361128;
MEDINE-9290785; PubMed=10361128;
MEDINE-9290785; Pactor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the the initiation of blood coagulation, fibrinolysis, and the the initiation of blood coagulation, fibrinolysis, and the the initiation of blood coagulation, fibrinolysis, and the the initiation of bradykinin and amgiotensin.

CC -1- CFALMYTIC ACTIVITY: Cleaves Selectively Arg-|-1le bonds in factor VII to form factor VII and factor XI to form factor XIa.

VII to AND MOLYCOSYLATED.

CC -1- DISEASE: Defects in F12 do not cause any clinical symptoms. The sole effect is that whole-blood clotting time is prolonged.

CC -1- DISEASE: Defects in F12 do not cause any clinical symptoms form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII and then to beta-factor XIIa. Alpha-factor CC XIIa activates factor XIIa.

CC -1- SIMILARITY: Contains 1 fibronectin type II domain.

CC -1- SIMILARITY: Contains 1 fibronectin type II domain.
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                                                                                                                                                                                                                                                                            "Coagulation factor XII Locarno: the functional defect is caused by the amino acid substitution Arg-353-->Pro leading to loss of a kallikrein cleavage site."; Blood 84:1173-1181(1994).
"Coagulation factor XII (Hageman factor) Washington D.C.: inactive factor XIIa results from Cys-571-->Ser substitution.";
Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
                                                                                                                                      VARIANT LOCARNO PRO-372.
MEDLINE-94325559; PubMed-8049433;
Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A., Furlan M.,
Laemmle B.;
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51 QBENTSSTLTHAENP---DWYYT----EDQ-------ADPC-QPNPCEHGGDCLV 90
              MIN, 2346001 - Feblood coaquiation factor XI activity, TAS.

DR GO; GO: 0003805; F: Piblood coaquiation factor XII activity, TAS.

DR GO; GO: 0003805; F: Piblood coaquiation factor XII activity, TAS.

DR GO; GO: 0003805; F: Piblood coaquiation factor XII activity, TAS.

DR GO; GO: 0000326; F: Piblood coaquiation.

DR InterPro: IPR000003; Fibrital.

DR InterPro: IPR000003; Fibrital.

DR InterPro: IPR000003; Fibrital.

DR InterPro: IPR000003; Fibrital.

DR InterPro: IPR000003; Fibrital.

DR InterPro: IPR000003; Fibrital.

DR InterPro: IPR000003; Fibrital.

DR Ffam; PF000005; First.

DR Ffam; PF000005; First.

DR Ffam; PF000005; First.

DR Ffam; PF000005; First.

DR FFAM; First.

DR FFAM; First.

DR FRINTS; FR00103; FIRTYEII.

DR FRINTS; FR00103; FIRTYEII.

DR FRANTS; FR00103; FIRTYEII.

DR SWART; SW00008; FRZ; II.

DR SWART; SW00008; FRZ; II.

DR SWART; SW000039; FRZ; II.

DR FROSTIE; F800023; FIRENGETIN.

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ALPHA-PACTOR XIIA LIGHT CHAIN.
BETA-PACTOR XIIA PART 1.
BETA-FACTOR XIIA PART 2.
PIBRONECTIN TYPE-II.
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FIBRONECTIN TYPE-I.
EGF-LIKE 2.
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                                                                            PYTGPSCSQVV-PVCRPNPCQNGATC---SRHKRRSKFTCACPDQFKGKFCEIGSD-DCY 195
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                                                                                                                                                                              -----GFDSCG-KTEIAERKIKRIYGGFKSTAGKHPWQASLQ 332
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                                                                                                                                                                                                                                                                                                                                         SGSE-CHISGWGVTETGKGSRQ----LLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNL 497
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                                                                                                                                                                                                                                                                                                                                                                                                 and TPA.";

Int. Dairy J. 5:605-617(1995).

-!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.

-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ravn P., Berglund L., Petersen T.E.; "Cloning and characterization of the bovine plasminogen activators uPA
                                                                                                                                                                                                                                                                                                            442 LAVRSYRLHEAFSPVSY-----QHDLALLRLQEDADGSCALLSPYVQPVCLPSGAARP
                                                                                                                                                                                                                                                                                                                                                       HGSTFTCSCLAPFSGNKCOKVQNTCKDNPCGRGQCL-----ITQSPPYYRCVCKH
                                                      MPŚGPHĆLĆPQHLTGNHĆQK-----EKĆFEPQLLRFFHKNEIWYRTEQAAVARĆQĆKG
                                                                                               166 P--DAHCORLASQACRINPCLHGGRCLEVEGHR-----LCHCPVGYTGPFCDVDTKASCY
                                                                                                                     VGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKP
                                                                                                                                        219 DGRGLSYRGLARTILSGAPCOPWASEATYR---NVTAEOARNWGLGGHAFCRNPDNDIRP
                                                                                                                                                                                                                                                    333 SSLPLTISMPQGH-FCGGALIHPCWVLTAAHCTDIK--TRHLKVVLGDQDLKK----EE
                                                                                                                                                                                                                                                                        ------wghsrcagsliarcwvltaahclodrrapedltvvlggerrnhscepcot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted; extracellular.
PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
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Sukaryota, Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                        TPA BOVIN STANDARD; PRT; 566 AA.
Q28198;
Q1907 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
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TISSUE=Kidney;
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                                                                                                                                                                                                               147 A--ECANWNSSGLAMKPYSGR------RPNAIRLG--LGNHN----YCRNPDQDSK 188
                                                                                                                                                                                                                                 ***---FK-----GKFCEIGS------DDCYVGDGYSYRGKMNRTVNQHACLYWNSHLL 223
                                                                                                                                                                                                                                                                                                             284 PEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQ 343
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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 02-FEB-2003 (Rel. 41, Last annotation update)
DF 28-FEB-2003 (Rel. 41, Last annotation update)
DF 30-FEB-2003 (Rel. 41, Last annotation update)
OC Bukaryots, Metascap Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.
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                                                                                                                 DB 1; Length 566;
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2EB6BEB4E32276C3 CRC64;
                                                                                                                                   68; Mismatches 179;
                                                                                                              Query Match 23.3%; Score 734.5; DB 1
Best Local Similarity 34.9%; Pred. No. 1.7e-44;
Matches 182; Conservative 68; Mismatches 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 PQGHFCGGALIHPCWVLTAAHCTDIK--TRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYS 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58; Gaps
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PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS50070; KRINGLE 2; 1.
PROSITE; PS50070; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PLasminogen activation; Hydrolase, Serine protease; Glycoprotein; Kringle; EGF-like domain; Signal; Multigene family.
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                                                                                                                                                                                                                                        SALIVARY PLASMINOGEN ACTIVATOR EGF-LIKE.
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Matches 157; Conservative
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FA12_BOVIN ID FA12_BOVIN STANDARD; AC D98140; T 01-FEB-1996 (Rel. 33, Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 16:2270-2278(1977).

Biochemistry 16:2270-2278(1977).

Le FUNCTION: Pactor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.

C. OTALNITC ACTIVITY: Cleaves selectively Arg-|-11e bonds in factor VII to form factor VII a and factor XI to form factor XII.

THISCELIAMBROUS: Factor XII, prekallikrehn, and HWW kininogen form a michoic surface. Prekallikrehn is cleaved by factor XII and then to beta-factor XIII a cleaved by factor XII a fortor XIII and then to beta-factor XIII a cleaved by factor XIII and then to beta-factor XIII a cleaved only to alpha-factor XIII as it lacks the trypsin/

C. SIMILARITY: Contains 2 EGF-like domains.

C. SIMILARITY: Contains 1 fibronectin type II domain.

C. SIMILARITY: Contains 1 fibronectin type II domain.
                                                                                                                                                                                                                                          MEDINE-4542782; PubMed=8186251;
Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;
Shibuya Y., Structure of bovine Hageman factor (blood coagulation factor
"Primary structure of bovine Hageman factor (blood coagulation factor
XII); comparison with human and guinea pig molecules.";
Biochim. Biophys. Acta 1206:63-70(1994).
                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDLINE=77182112; PubMed=861210;
Fujikawa K., Walsh A.K., Davie W.E.;
"Isolation and characterization of bovine factor XII (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR009003; Cys_Ser_trypsin.
Interpro; IPR006209; EGF_like.
Interpro; IPR000639; Fibracini.
Interpro; IPR000545; FN Type_II.
Interpro; IPR006210; IEGF.
Interpro; IPR001209; Peptidase_SI.
Interpro; IPR001214; Peptidase_SI.
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Pfam; PF00009; fn1; 1.
Pfam; PF00004; fn2; 1.
Pfam; PF00009; kringle; 1.
Pfam; PF00089; krypsin; 1.
PRINTS; PR0072; CHYMOTRYPSIN.
PRINTS; PR0013; FNTYPEII.
PRINTS; PR00195; FNTYPEII.
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PIR; S45281; S45281.
HSSF; P00763; 1DPO.
                                                                                                    taurus (Bovine)
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SECOND S	h Similarity 33.0%; Pred. No. 1.7e-42; 91; Conservative 69; Mismatches 183; Indels 135; Gaps 31;	SSTLTHAENPDWYYTEDQADPC-QPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKV 111	ONTCKDNPCGRGQCLITQSPPYXRCVCKHPYTGPSCSQVV 151	PVCRPNPCQNGATCSRHKRRSKFTCACPDQFKGKFCEIG-SDDCYVGDGYSYRGK 205
Prodom; PR SMART; SM SMART, SM SMART, SM SM SM SM SM SM SM SM SM SM SM SM SM	Query Match Best Local Matches 193	R 9	112	152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 AGTILSGAPÇQSWASEATY---WNVTAEQVLNWGLGDHAFCRNPDNDTRPWCFI-WKGDR 276
                                                                                                                        360
                                                                                                                                                                                                         AHCTDIK--TRHLKNVLGDQDLKKEEFHEQS-----FRVEKIFK---YSHYNER 404
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P98119;
01-FF81-1996 (Rel. 33, Created)
01-FF8-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
                                                                        266 VKWEYCDVSAC--SAQDVAYPEESP-----TEPSTKLPGFDS--CGKTEIAE-----
                                                                                                                                                                                                                                                                                                                      ----RK----IKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA
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"Plasminogen activators from the saliva of Desmodus rotundus (common "Plasminogen activators from specificity.";
Vampire bat): unique fibrin specificity.";
Ann. N.Y. Acad. Sci. 667:395-403(1992).
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TISSUE-Salivary gland;
MEDLINE-2203936; PubMed=1937019;
Kraetzschmar J., Haendlar B., Langer G., Boidol W., Bringmann P., Alagon A., Donner P., Schleuning W.D.;
The plasminogen activator family from the salivary gland of the vampire bat Desendus rotundus: cloning and expression.";
Gene 105:229-237(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desmodus rotundus (Vampire bat).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Chiroptera; Microchiroptera; Phyllostomidae;
Desmodontinae; Desmodus.

NCBI_TAXID=9430;
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CHARACTERIZATION.
MEDLINE=93393059; PubMed=1309059;
Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
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551 TPERQLILRGIVSWGSGCGNRLKFGVYTDVANYLAWIR 588
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VLTAAHC--TDIKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDEIPHNDIAL 414
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                                                                                                                                                                                                                                                                                                                                                                                                                  178 CPDQFKGKFCEIGS-DDCYVGDGYSYRGKMANRTVNQHACLYWWSHLLLLQENYNMFMEDAE
                                                                                                                                                                                                                                                                                                                                                                                                                          120 CGRGOCLITOSPPYYRCVCKHPYTGPSCSQVVPV--CRPNPCQNGATCSRHKRRSKFTCA
                                                                                                                                                                                                                                                                                                                                                           Query Match
22.3%; Score 704.5; DB 1; Length 477;
Best Local Similarity 35.9%; Pred. No. 1.8e-42;
Matches 161; Conservative 64; Mismatches 160; Indels 63
                                                                                                                                                                                                                                                                                                                                               53616 MW; AA06FD1739C10E5E CRC64;
                         N-LINKED (GLCNAC. ..).
/FTId=CAR 000027.
N-LINKED (GLCNAC. ..).
/FTId=CAR_000028.
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration the Eurench should be considered through a collaboration the Buropean Bioinformatics finatitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       the presence of fibrin I.

-!- SUBUNIT: Monomer.
-!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced stimulation of activity.
-!- SIMILARITY: Belongs to peptidase family $1.
-!- SIMILARITY: Contains I EGF-like domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
-!- SIMILARITY: Contains I fibronectin type I domain.
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us-09-912-559-3.rsp

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267 VLTAAHCFQESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFD--DDTYNNDIAL 324
                                                               LKLKPVDGHCALESKYVKTVCLPDGS--FPSGSECHISGWGVTETGKG--SRQLLDAKVK 470
                                                                                     325 LOLKSDSPOCAQESDSVRAICLPEANLOLPDWTECELSGYGKHKSSSPFYSEQLKEGHVR 384
                                                                                                                                            471 LIANTLCNSRQLYDHMIDDSMICAGNLQK----PG-QDTCQGDSGGPLTCEKDGTYYVYG 525
                                                                                                                                                                   385 LYPSSRCAPKFLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLG 444
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
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STRAIN=Fischer 344;
MEDLINE=Fischer 344;
MEDLINE=Fischer 344;
Henderson B.R.,
Henderson B.R.,
Kefford R.F.;
Transcriptional and posttranscriptional activation of urokinase
plasminogen activator gene expression in metastatic tumor cells.";
Cancer Res. 52:2489-2496(1992).
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Pept S1A uPA.
Peptidase_S1.
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Interpro; IPRO09003; C)
Interpro; IPRO066209; E)
Interpro; IPRO06010; II
Interpro; IPRO000011; K;
Interpro; IPRO01593; F
Interpro; IPRO01593; F
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                  R Pfam; PF00051; kringle; 1.

R Pfam; PF00089; trypsin; 1.

R PRINTS; PR8C07122; CHYMOTRYPSIN.

R PRINTS; PR8C07122; CHYMOTRYPSIN.

R PRINTS; PR8C07123; CHYMOTRYPSIN.

R PRODOTS; CHYMOTRYPSIN.

R PRODOTS; CHYMOTRYPSIN.

R SMART; SM00181; EGF; 1.

R SMART; SM00181; EGF; 1.

R RPGSITE; PS00122; EGF 1; PALSE_NEG.

R RPGSITE; PS00121; KRINGLE 1; 1.

R RPGSITE; PS00121; KRINGLE 2; 1.

R RPGSITE; PS00121; KRINGLE 2; 1.

R PROSITE; PS00121; KRINGLE 2; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN LSER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

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R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

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R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

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R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PROSITE; PLAN SER; 1.

R PROSITE; PROSITE; PLAN SER; 1.
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CONNECTING PEPTIDE.
SERING PROTESSE.
BY SIMILARITY.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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E -> G (IN REF. 2).
D -> N (IN REF. 2).
4EB1B96C716244C8 CRC64;
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SHORT A CHAIN (A1) (BY
CHAIN B (BY SIMILARITY)
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interPro; IPR001314; Peptidase_S1A
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Best Local Similarity 37.9%
Matches 157; Conservative
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us-09-912-559-3.rsp

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Ā
Zymogen; Signal.
BY SIMILARITY
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005589; Q28209;
01-FEB-1994 (Rel. 28, Last seq. 28-FEB-2003 (Rel. 41, Last ann
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 domain;
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155; Conserv
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EGF-like
                                503
Kringle; |
SIGNAL
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DISULPID
ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85087954; PubMed-6096832;
Nagamine Y., Pearson D., Altus M.S., Reich E.;
"CDNA and gene muleotide sequence of porcine plasminogen activator.";
Nucleic Acids Res. 12:9525-9541(1984).
                                     20-MAR-1987 (Rel. 04, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
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PROSITE; PSSOOC21; KRINGLE 1; 1.
PROSITE; PSSOO70; KRINGLE 2; 1.
PROSITE; PSSO240; TRYPSIN DOM; 1.
PROSITE; PSOO134; TRYPSIN HIS; 1.
PROSITE; PSOO135; TRYPSIN SRN, 1.
PROSITE; PSOO135; TRYPSIN SRN, 1.
PROSITE; PSOO135; TRYPSIN SRN, 1.
                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                    DSGGPLTCEKDGTYYVYGIVSWGLECGK--RPGVYTQVTKFLNWIKATIKSESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1986) to the PIR data bank.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; SU1.231, 1.
InterPro; PR0005003; Cys Ser trypsin.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR001254; Pept dase_S1.
InterPro; IPR001254; Pept dase_S1.
InterPro; IPR001314; Pept dase_S1.
Pfam; PF00069; trypsin; 1.
Pfam; PF00069; trypsin; 1.
PRNTS; PR00722; CHYMOTRYPSIN.
PRNTS; PR000129; KRINGLE.
ProDom; PD00039; KRINGLE.
ProDom; PD00039; KRINGLE.
PROBITE; PS001030; KR; 1.
PROSITE; PS01166; EGF 2; PALSE_NEG.
PROSITE; PS01166; EGF 2; PALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X01648, CAA25806.1, --
EMBL, X02724, CAA26511.1, --
PIR, A00932, UKPG.
MESSP, P00749, 1KPU.
MEROPS, S01.231, --
                                                                                                                                           STANDARD;
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                                                                                                       RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONGATCSRHKRRSKF-TCACPDQFKGKFCEIG-SDDCYVGDGYSYRGKMNRTVNQHACL 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 ----YRRHRGGSVTYVCGGSLISPCWVVSATHCFINYQQKEDYI-VYLGRQTLHSSTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 EQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 YWNSHLLLQENYNMFWEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSAC
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
UROKINASE-TYPE PLASMINOGEN ACTIVATOR
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                                                                                                                                                                                         SERINE PROTEASE.

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INTERCHAIN (BY SIMILARITY).

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; Pred. No. 3.3e-41;
63; Mismatches 169; Indels
                            CHAIN A (BY SIMILARITY)
CHAIN B (BY SIMILARITY)
                                                                                                                          KRINGLE.
CONNECTING PEPTIDE.
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28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor
(U-plasminogen activator).
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SV-----GKSPSSPREKEE--FQCGQKALRPR--PKIVGGQVTNAENQPWFAAIYRRHR 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204. GGSIT-----YLCGGSLISPCWVVSATHCFIDHPKKBNYIVYLGQSRLNSDTRGEMQ 255
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INTERCHAIN (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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21.7%; Score 683.5; DB 1; Length 433;
Best Local Similarity 36.7%; Pred. No. 4.9e-41;
Matches 152; Conservative 66; Mismatches 161; Indels 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | REBL; L03546; AAA51419.1; | REBL; X65801; CAA59796.1; | REBL; X65801; CAA59796.1; | REBL; X65801; CAA59796.1; | REBL; X65801; CAA59796.1; | REBL; X65801; CAA59796.1; | REBL; X65801; CAA59796.1; | RESP; PO0749; ILMW. | REOPS; S01.231, | REOPS; S01.231, | REOPS; S01.231, | REOPS; S01.231, | REOPS; REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR | REPORTOR 
                                                                                                                                                                                                                                                                                                   UROKINASE-TYPE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                               "Bovine urokinase-type plasminogen activator and its receptor: cloning and induction by retinoic acid."; Gene 125:177-183(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Int. Dairy J. 5:605-617(1995).
-!-CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond plasminogen to form plasmin.
-!- INDUCTION: By retinoic acid.
-!- SIMILARITY: Belongs to peptidase family $1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.
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MEDLINE-93216119; PubMed-8385052;
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Schleuning W.-D.,
                Bovidae, Bovinae, Bos
NCBL_TaxID=9913;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

May 24, 2004, 09:43:35; Search time 39 Seconds (without alignments) 4530.518 Million cell updates/sec Run on:

OM protein - protein search, using sw model

US-09-912-559-3 3154 1 MFARMSDLHVLLLMALVGKT......TQVTKFLNWIXATIKSESGF 560 Title: Perfect score: Sequence:

Scoring table:

1017041 seqs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SPTREMBL 25:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q14520 homo sapien	Q8k0d2 mus musculu	Q800y7 meleagris g	Q8vcs4 mus musculu	Q9bu99 homo sapien	Q86yk8 homo sapien	Q8sq23 sus scrofa	Q8mkbl oryctolagus	Q8izz5 homo sapien	097507 sus scrofa	Q9bzwl homo sapien	O35727 mus musculu	Q80yc5 mus musculu	Q8mil0 oryctolagus	Q8mhy7 oryctolagus	Q15146 homo sapien
SUMMARIES		QI	Q14520	Q8K0D2	Q800Y7	Q8VCS4	66DE60	Q86YK8	Q8SQ23	Q8MKB1	Q8IZZ5	097507	Q9BZW1	035727	Q80YC5	QBMILO	Q8MHY7	Q15146
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	, 2	Match	100.0	74.9	26.3	26.3	24.3	24.3	24.0	23.4	23.1	23.0	22.6	22.0	21.8	21.2	21.1	20.3
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RQ); GO: 0007155; P: cell addresion; TAS.

RICEPPO: IPRO00001; Cys Ser trypsin.

RICEPPO: IPRO00001; Kringle.

RICEPPO: IPRO01254; Peptidase_S1.

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N RESULT Q8K0D2

129 189 146 249 DADEKEWGEIKUTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDSCGKTEIAER 309 69 86 10 VILLMALVGKTACGFSIMSILESLDPDWTPDQYDYSYEDYNQEENTSSTLTHAENPDWYY 70 TEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPCGRGQCLITQ 32 -----DPCQSNPCEHGGDCIIRGDTFSCSCPAPFSGSRCQTAQNKCKDNPCVHGDCLIIQ 130 SPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPDQFKGKFCEI 87 KHPYYRCACKYPYTGPDCSKVLPACRPNPCQNGGVCSRHRRRSRFTCACPDQYKGKFCEI 190 GSDDCYVGDGYSYRGKAMRTVNQHACLYWNSHLLLQENYNWFMEDAETHGIGEHNFCRNP Gaps 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (TEL TaxID=10090; 517; 39; DB 11; Length 63; Indels 6 VLLLIALVGKSVIGLSLMSFIAPPDP---------Query Match

Rest Local Similarity 75.1%; Pred. No. 2.6e-209;
Matches 413; Conservative 35; Mismatches 63; 250

148 131

80 86

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us-09-912-559-3.rsp[†]

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-FPSGSECHISGWGVTE---TGKGSRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGN 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 NRIVNQHACLYWNSHLLLQENYNMFMEDABIHGIGEHNFCRNPDADEKPWCFIKVTNDKV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 KHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHC--TDIKTRHLKVVLGDQDLK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHPWTAAIYIG------ESPCAGTLIQTCWVVSAAHCFANSPOKSSIKVVLGQHFFN 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 RVEHKSCVHDPCMNGGECKMIASSGKTVCDCKGPFVGKYCNIVPNHHCYRGNGTEYRGTA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 KTTISGHSCLPWNSDLLYRELHVDSVEKAVQLGLGPFSYCRNPDEDEKFWCYI-MKDNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDSK-SDACQGDSGGFLACENNEISYLYGVISWGDGCGRVNKFGVYTRVPNYVNWINERI
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLAPFSGNKCOKVONTCKDNPC------GRGQCLITQSPPYYRCVCKHPYTGPSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPEEFTGRDCQ--MXKCFDDSLYEFFDVDMRWSR-----VKQGSVEQCICVDGQM--ECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 KWEYCDVSACSAQDVAYP--EESPTEPSTKLPGFDSCGKTEIAERKIK-RIYGGFKSTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 SWEYCNITSCASRERRPPVLEDIDTFAVPRRP----CGRRHKKRSFVRPRIIGGSSSLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 RITDVĮQIFEIEKYILYPQYSVFRPTEH-DIALIKLKKNGQRCAVKSQFVQPICLPESNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDYNQEENTSSTLTHAENPD - WYY - - - TEDQADPCQPNPCEHGGDC - LVHG - STFTCS
                                                                                                                                                                                                                                                                                                                                                                      149 OVV-PVCRPNPCQNGATCSRHKRRSKFTCACPDQFKGKFCEI-GSDDCYVGDGYSYRGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 KEEFHEQSFRVEKIFKYSHYNBRDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPDGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                             540;
                                                                                                                                                                                                                                        26.3%; Score 831; DB 13; Length 5 llarity 34.8%; Pred. No. 7.4e-68; Conservative 86; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL, BC019376; AAH19376.1;
-HSSP: P00761; IANI.
GO, GO:0005576; C:extracellular; IEA.
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540 540
540 AA; 61159 MW; OBB3B4A89COB577F CRC64;
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Last sequence update)
Last annotation update)
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                     | PS00021; KRINGLE 1; 1. | PS50070; KRINGLE 2; 1. | PS500240; TRYPSIN DOM; 1. | PS00134; TRYPSIN HIS; 1. | PS00135; TRYPSIN SER; 1.
FIBRONECTIN 1; 1.
KRINGLE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR.2002 (TrEMBLrel. 20, 01-MAR.2002 (TrEMBLrel. 20, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 188; Conserv
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  PS01253;
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Q8VCS4;
01-MAR-2002 (
PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE;
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                                                                                    HLKVVLGDQDLKKEEPHEQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESK 429
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  207 DGDHKPWCFVKVNSEKVKWEYCDVTVCPVPDTPNPVESLLEPVMELPGFESCGKTEVAEH 266
                                                                                                                                                                                                                                                                               387 YVKTVCLPSDPFPSGTECHISGWGVTETGEGSRQLLDAKVKLIANPLCNSRQLYDHIDD
                                                                                                                                                                                                                                                                                                                                                                           310 KIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHCTDIKTR
                                                                                                                                                                                                                                                  YVKTVCLPDGSFPSGSECHISGWGVTETGKGSRQLLDAKVKLIANTLCNSRQLYDHMIDD
                                                                                                                                                                                                                                                                                                                                                    SMICAGNIOKPGODICOGDSGGPLICEKDGTYYVYGIVSWGLECGKRPGVYTQVTKFLNW
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocyte growth factor activator (Fragment).
Moleagris gallopavo (Common turkey).
Moleagris gallopavo (Common turkey).
Archosauria, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria, Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
NIBI_TAXID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22122796; PubMed=12128063;
MEDLINE=22122796; PubMed=12128063;
MEDLINE=22122796; PubMed=12128063;
"Expression of a hepatocyte growth-factor activator protein (Meleagris gallopavo) deferent duct epithelial cells.";
[Capp. Biochem. Physiol. 132:769-777(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N 121

A SEQUENCE FROM N.A.

A Holsberger D.R., Becker A.E., Thurston R.J., Rice C.D.;

L Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AV216598, AA046038.1; --

R GO; GO:0006263; F:Crymotrypsin activity; IEA.

R GO; GO:0006263; F:Crymotrypsin activity; IEA.

R GO; GO:0006263; F:Crymotrypsin activity; IEA.

R GO; GO:0006263; F:Crymotrypsin.

R GO; GO:0006263; F:Crymotrypsin.

R InterPro; IPR00903; Cys_Ser_trypsin.

R InterPro; IPR0000742; EGF_1ke.

R InterPro; IPR0000742; EGF_1ke.

R InterPro; IPR0000562; F:Crymotrypsin.

R InterPro; IPR0001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

DR RIMYS; PR001254; CHYMOTRYSIN.

DR PRIMYS; PR00125; CHYMOTRYSIN.

DR PRIMYS; PR00125; CHYMOTRYSIN.

DR PRIMYS; PR001395; Kringle; 1.

DR SWART; SM00186; FN1; 1.

DR SWART; SM00186; FN1; 1.

DR SWART; SM00130; Tryp_SPC; 1.

DR PROSITE; PS01186; EGF_2; 1.
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Q800Y7
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323 306

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77 COPNECEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP--CGRG----- 123
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                                                                                          632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
40 CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYRGTWSTAESG
                                                                          574 DISPNMLCAGYFDCK-SDACQGDSGGPLVCEKNGVAYLYGIISWGDGGGRLNKPGVYTRV
                                                       486 MIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDGTYYVYGIVSWGLECGK--RPGVYTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strauberg R.;
Strauberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to PEPTIDASE FAMILY SI.
- - SIMILARITY: CONTAINS 2 KRINGLE DOWAINS.
DR GO: 00004295; AAH02795.1; - .
RSSP; POOTO60; JASH.
GO; GO:0004295; F: tryppsin activity; IEA.
GO; GO:0004295; F: tryppsin activity; IEA.
GO; GO:0004295; F: tryppsin activity; IEA.
GO; GO:0004295; F: tryppsin activity; IEA.
GO; GO:0004295; F: tryppsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0004295; F: trypsin; IEGF_IX.
INTERPROSID: PROMO124; Peptidase_SI.
INTERPROSID: RANGLE.
FROMO139; RKNOLE.
FROMO139; RKNOLE.
FROMO139; RKNOLE.
FROMO139; RKNOLE.
FROSITE; PSOU020; Tryp Sec; I.
FROSITE; PSOU021; KRINGLE_2; Z.
SWART; SMO0139; RKNOLE.
FROSITE; PSOU021; KRINGLE_2; Z.
FROSITE; PSOU014; TRYPEIN HIS; I.
FROSITE; PSOU014; TRYPEIN HIS; I.
FROSITE; PSOU014; TRYPEIN HIS; I.
FROSITE; PSOU014; TRYPEIN HIS; I.
FROSITE; PSOU014; TRYPEIN HIS; I.
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24.3%; Score 766.5; DB 4; Length 5:
Best Local Similarity 35.0%; Pred. No. 6.2e-62;
Matches 182; Conservative 77; Mismatches 176; Indels
                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to plasminogen activator, tissue.
Homo saplens (Human)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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633 ANYVDWINDRIR 644
                                                                                                                                  544 TKFLNWIKATIK 555
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease
SEQUENCE 516 7
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Q9BU99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 GKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 GVASTAASGLSCLAMNSDLLYQELHVDSVAAAVLLGLGPHAYCRNPDKDERPWCYV-VKD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKVKWEYCDVSACSAQD-----VAYPEESPTEPSTKLPGFDSCGKTEIAERKIK- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIYGGFXSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHC--TDIKTRH 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKVVLGDDDLKKEEFHEQSFRVEKIFKYSHYNERDEIPHN-DIALLKLKPVDGHCALESK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVKTVCLPD--GSFPSGSECHISGWGVTE--TGKGSRQLLDAKVKLIANTLCNSRQLYDH 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 KDCG--TEKCFDETRYEYFEVGDHWARVSEGHVEQCG---CMEGOA----RCEDTHH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 PSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPDQFKGKFCEI-GSDDCYVGDGYSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 THAENPD--WYYTEDQA-----DPCOPNPCEHGGDCLV---HGSTFTCSCLAPFSG
 Query Match
26.3%; Score 829; DB 11; Length 653;
Best Local Similarity 34.4%; Pred. No. 1.4e-67;
Matches 190; Conservative 79; Mismatches 187; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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us-09-912-559-3.rspt

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T-plasminogen activator.
Sus scrofa (Pig).
Sukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
(VCBI_TaxID=9823;
                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                     77 COPNECEHGGDC--LVHGSTFTCSCLAPFSGNKCO-KVQNTCKDNP--CGRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
24.3%; Score 765.5; DB 4; Length
Best Local Similarity 35.0%; Pred. No. 8.6e-62;
Matches 182; Conservative 76; Mismatches 177; Indels
PROSITE; PS50070; KRINGLE_2; 2.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SEQUENCE 562 AA; 62902 WW; 837D98392F6EDDIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8SQ23 PRELIMINARY; PRT; 562 AA. Q8SQ23; Q8SQ23; Careber 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2003 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            124
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                                                                                                                                                                                                                                                                                           QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG----QDTCQGDSGGPLTCEK 517
        146
                                                                                                                                                                                                                                                                                                                                                               349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEBFHEQSFRVEKIFKYSHYNERDE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR 462
                                                                                                                                                         229 NWFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP
                                                                                                                                                                                     204 TAQNPSAQALGLGKHNYCRNPDGDAKPWCHV-LKONRRLTWBYCDVPSCS------
        -----RPDAIRLGLGNHNYCRNPDRDSKPWCYV
                                                                                      ---FRAGKYSBEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY
                                                                                                                                                                                                                                                             289 TEPSTKLPGFDSCGKTBIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG
                                                           PDQFK-GKF-----CEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QB6YK8;

QB6YK8;

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

01-JUN-2003 (TrEMBLrel. 25, Last annotation update)

11ssue plasminogen activator.

Tissue plasminogen activator.

Eukaryota; Metazoa; Conordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NICLIANT, AND CALL, ZENG Y., HE X.;

Liu Y., Xii L., ZENG Y., HE X.;

Liu Y., Xii L., ZENG Y., HE X.;

Liu Y., Xii L., ZENG Y., HE X.;

Liu CDNA, O't Lissue plasminogen activator.";

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:000556; C:extracellular; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; F:trypsin activity; IEA.

GO; GO:0006508; F:trypsin activity; IEA.

GO; GO:0006509; F:procellular.

R GO; GO:0006509; F:procellular.

InterPro; IPR000003; CYS Ser_trypsin.

InterPro; IPR000001; Kringle.

InterPro; IPR000001; Kringle.

InterPro; IPR00114; Peptidase_S1.

R InterPro; IPR00114; Peptidase_S1.

R Pfam; PR00003; fful; 1.

P Ffam; PR00003; fful; 1.

P Ffam; PR00009; Kringle; 2.

P Ffam; PR00009; KR: II.

R PRINTS; PR00120; KR: II.

P RNNTS; PR00130; KR: II.

R PROSTITE; PS01186; EGF_1:

R PROSTITE; PS01186; EGF_2:

R PROSTITE; PS01186; EGF_2:

R PROSTITE; PS01186; EGF_2:

R PROSTITE; PS01186; EGF_2:

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R PROSTITE; PS01186; EGF_2:

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             AECTINWINS ---- SALAQKPYSGR --
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                                                     145
                                                                               178
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                         123
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                                                                                                                                                                                                                                                                                                                                401
                                                                                                                                                                                                                                                                                                                                                                                                                                463 QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTCEK
                                                                                                                                                                                                                                                                 349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDE
                                                                                             146 AECTNWNS----SALAQXPYSGR------RPDAIRLGLGHNYCRNPDRDSKPWCYV
                                                                                                                                   179 PDQFK-GKF-----CEIGSDDCYVGDGYSYRGKWARTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                         289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG
                                                                                                                                                                                                                                                                                                                      -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC
                                                                                                                                                     Gaps
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BDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPS 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 A--OCVNWNSSWLALKPYSGR------KPNALRIGLGNHNYCRNPDRDTKPWCYVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 AGTYSPEFCSTPACSKEKNGNCYLGKGQAYRGTHSLTTSGASCLFWNSMLLVGEKYTARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 PYYRCV-----CKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 PDQFKGKFCEI-----GSDDCYVGDGYSYRGKWNRTVNQHACLYWNSHLLLQENYNMFM
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                                                                                          01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last sequence update)
Tissue-type planinogen activator.
Chyctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleii; Lagomorpha; Leporidae; Oryctolagus.
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PROSITE; PS00134; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_BIS; 1.
PROSITE; PS00135; TRYPSIN_BER; 1.
PROSITE; PS00135; TRYPSIN_BER; Hydrolase; Kringle; Protease;
                                                                                                                                                                                                                                                                                                                                                                             23.4%; Score 737; DB 6; Length 56
35.5%; Pred. No. 3.7e-59;
ive 73; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 AA; 62726 MW; 459D8BAC6D4A937C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SM00020; Tryp_SPC; 1.
TE; PS00022; EGF_1; 1.
TE; PS01186; EGF_2; 1.
TE; PS01253; FIBRONECTIN 1; 1.
TE; PS00021; KRINGLE_1; 2.
TE; PS50070; KRINGLE_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN DOM; 1.
TRYPSIN HIS; 1.
TRYPSIN SER; 1.
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Pfam; PF000039; fn1; 1.
Pfam; PF000051; Kringle; 2.
Pfam; PF00089; trypain; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 2.
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SMART; SM00058; FN1; 1
SMART; SM00130; KR; 2.
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SEQUENCE 564 7
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Best Local S:
Matches 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 YQQHQSWLRPLLRGNRVEHCWCNDGQTQCHSVPVKSCSEPRCFNGGTCLQAIYFSDFVCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 CLAPFSGNKCQ-KVQNTCKDNP--CGRGQCLITQSPPYYRCV-----CKHPYTGPSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RPDAVKLGLGNHNYCRNPDKDSKPWCYIFKAEKYSPDFCSTPACTKEKEECYTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 HV-LKDHKLTWEYCDLPQCV--------TKGLRQYKEPQF-RIKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 QVVPVCRPNPCQ----NGATCSRHKRRSKFTC-----ACPDQFKGKFCEIGSDDCYVG
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                                                                                                                                                                                                                                                                                                                                        R SMART; SM00181; EGF; 1.

R SMART; SM00185; FN1; 1.

R SMART; SM00185; FN1; 1.

R SMART; SM00180; KR; 2.

R SMART; SM00180; KR; 2.

R PROSITE; PS00122; EGF 1; 1.

R PROSITE; PS0125; FIRENBURCIN 1; 1.

R PROSITE; PS00121; KRINGLE 1; 2.

R PROSITE; PS00121; KRINGLE 2; 2.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00137; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.

R PROSITE; PS00136; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%; Score 758.5; DB 6; Length 33.5%; Pred. No. 3.8e-61; ive 80; Mismatches 201; Indels
                                                                                            InterPro; IPR000001; Kringle.
InterPro; IPR001244; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRPSIN.
PRINTS; PR00722; CHYMOTRPSIN.
IPR009003; Cys Ser trypsin.
IPR006209; EGF_11kE.
IPR000083; Fibrnctn1.
IPR006210; IEGF.
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Best Local Similarity 33.5%;
Matches 183; Conservative
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                                                                                293 TKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHF-CGGAL 351
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                                                                                                                                                                                                                                                                                           NDIALLKLKPVDGHCALESKYVKTVCLPDGS--PPSGSECHISGWGVTE--TGKGSRQLL
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Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;
Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;
Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;
Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;
Wada Goldon R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., Remander R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homó sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HILIGIISWGLGCGOKDVPGVYTKVVNYLGWIQ 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521 YYVYGIVSWGLECGKR--PGVYTQVTKFLNWIK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PP00040; fn2; 1.
Pfam; PP00051; kringle; 1.
Pfam; PP00069; kringle; 1.
PRINTS; PR00122; CHYMCTRYPSIN.
PRINTS; PR001013; FNTYPEII.
PRINTS; PR001013; FNTYPEII.
PRODOM; PD0000995; FNTNGLE.
PRODOM; P00000995; FNTNGLE.
SWART; SW00199; EGF; 2.
SWART; SW00059; FNI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tryp_SPc; 1.; EGF_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Coagulation factor XII-Mie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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SMART; SM00059; FN1; 1.
SMART; SM00059; FN2; 1.
SMART; SM00130; KR; 1.
SMART; SM000120; Tryp SPC
PROSITE; PS00022; EGF 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00008, EGF, 2.
Pfam, PF00039, fnl, 1.
Pfam, PF00040, fnl, 1.
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FHEQSFRVEKIFKYSHYNERDEIPHNDIALLKL-KPVDGHCALESKYVKTVCLPDGSF-P 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 MPSGPHCLCPQHLTGNHCQK-----BKCPEPQLLRFFHKNEIWYRTEQAAVARCQCKG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 SSLPLTISMPQGH-FCGGALIHPCWVLTAAHCTDIK--TRHLKVVLGDQDLKK----EE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 WCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPT----------EPSTKL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GFDSCG-KTEIAERKIKRIYGGFKSTAGKHPWQASLQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKPGQDICQGDSGGPLICEKDGI---YYVYGIVSWGLECGKR--PGVYTQVIKFLNWIK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610
                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                          53 YHRQLYHKCTHKGRPGPQPWCATTPNPDQDQRWGYCLEPKKVKDHCSKHSPCQKGGTCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 DGRGLSYRGLARTTLSGAPCQPWASEATYR---NVTAEQARNWGLGGHAFCRNPDNDIRP
                                                                                                                                                                                                                                                                                                                                                                 1 MRALLLL------GFLLVSLESTLSIPPWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQ
                                                                                                                                                                                                                                                                                                                                                                                                          QEENTSSTLTHAENP---DWYYT-----EDQ------ADPC-QPNPCEHGGDCLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGSTFTCSCLAPFSGNKCQKVQNTCKDNPCGRGQCL-----ITQSPPYYRCVCKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 PYTGPSCSOVV-PVCRPNPCQNGATC---SRHKRRSKFTCACPDQFKGKFCEIGSD-DCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P--DAHCORLASQACRINPCLHGGRCLEVEGHR-----LCHCPVGYTGPFCDVDTKASCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 VGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNWFWEDAETHGIGEHNFCRNPDADEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - GATDACQGDSGGPLVCEDQAAERRLTLQGIISWGSGCGDRNKPGVYTDVAYYLAWIR
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                         Indels 164;
                                                                                                                                                                                                                             Length
PS01186; EGF 2; 1.
PS0123; FIBRONECTIN 1; 1.
PS00023; FIBRONECTIN 2; 1.
PS00021; KRINGLE 1; 1.
PS50070; KRINGLE 2; 1.
PS50240; TRYPSIN DOM; 1.
PS00135; TRYPSIN HIS; 1.
PS00135; TRYPSIN SER; 1.
PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                     8 LHVLLLMALVGKTACGFSLMSLLESLD-PDW-TPDQYDYSYED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                             23.1%; Score 728; DB 4; Lo
31.1%; Pred. No. 2.8e-58;
iive 79; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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(TrEMBLrel. 10, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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405
                                                                                                                                                                                              357 VLTAAHCTDIK--TRHLKVVLGDQDLKKEEFHE-----QSFRVEKIFKYSHYNERDEIP 408
                                                                                                                                                                                                                                    409 HNDIALLKLK-PVDGHCALESKYVKTVCLP----DGSFPSGSECHISGWGVTETG--KGS 461
296 QAPIGEAPPILIPIQSPSEHQDSPLLSREPQPTIQIPSQNLTSAWCAPPEQRGPLPSAGL 355
                                                                                                       356 VGCCG-RIEKKLSSLNRIVGGLVALPGAHPYIAALYWG------QNFCAGSLIAPCW
                                                                                                                                                                                                                                                                                                                                                                        299 DSCGKTEIAER--KIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 RQLLDAKVKLJANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN. 2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Neonatal thrombolytic agent alpha-form (Fragment).
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P DOU D.;

"A brain-type plasminogen activator.";

"A brain-type plasminogen activator.";

"I brain-type plasminogen activator.";

"I brain-type plasminogen activator.";

"I submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

"I similarity: EELONGS TO PEPTIDASE FAMILY SI.

"I SIMILARITY: CONTAINS I KRINGLE DOWAIN.

R HSSP; POOTSO; LESS AAKI1956.1; -.

R HSSP; POOTSO; LESS AAKI1956.1; -.

R GO; GO:000525; R P:peptidase activity; IEA.

R GO; GO:0004263; F:peptidase activity; IEA.

R GO; GO:000526; F:peptidase activity; IEA.

R GO; GO:0005083; F:peptidase SI.

R InterPro; IPR00083; F:peptidase SI.

InterPro; IPR000134; Peptidase SI.

R InterPro; IPR00134; Peptidase SIA.

P Fam; PR00089; trypsin; I.

P Fam; PR000189; trypsin; I.

R PRINTS; PR000189; KR:ingle; I.

R SMART; SM00026; RR; I.

R SMART; SM00020; TRYP SPC; I.

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; KR:INLEL;

R PROSITE; PS01021; RR:INLEL;

R PROSITE; PS01021; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 RQLVLRGİVSWGSGGBRLKPGVYTDVANYLAWİQ 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 -- YYVYGIVSWGLECGKR--PGVYTQVTKFLNWIK 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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SEQUENCE FROM N.A.
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Q9BZW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 -----EKCFEPQFLQFFQENEIWHRPEPAGVSKCQCKGPKA--QCKPVASQVCSTNPCL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 YWNSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSAC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 SSTLTHAENPDWYYTEDQ----ADPC-OPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCOKV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 NGGSCLQTEGHR----LCRCPTGYAGRLCDVDLXERCYSDRGLSYRGMAQTTLSGAPCQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 PWASEATY---WMMTAEQALNWGLGDHAFCRNPDNDTRPWCFV-WRGDQLSWQYCRLARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 NGATCSR---HKRRSKFTCACPDQFKGKFCEIG-SDDCYVGDGYSYRGKMNRTVNQHACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS0103; FIBRONECTIN 1; 1.
PROSITE; PS00023; FIBRONECTIN 2; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS0001; KRINGLE 2; 1.
PROSITE; PS50070; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SRR; 1.
EGF-like domain; Glycoprofein; Hydrolase; Kringle; Protease;
                                             Takahashi T., Kihara T.;

"Procrime liver factor XII.";
"Procrime liver factor XII.";
"Porcine liver factor XII.";
"Le Siminarity: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS I KRINGLE DOMAIN.

C. -!- SIMILARITY: CONTAINS I KRINGLE DOMAIN.
RESP: PO0763; 1DPO.
RESP: P00763; 1DPO.
RESP: P00763; 1DPO.
RESP: P00763; 1DPO.
RESP: P00763; 1DPO.
RESP: P00763; 1DPO.
RESP: P00763; 1DPO.
RESP: P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SAQDVAYPEESPTE------PSTKLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001219, ISBN InterPro; IPR0012194; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Fam; PP00009; EGF; 2.
Fam; PP00039; fn1; 1.
Fam; PP00051; Kringle; 1.
Fam; PP00081; trypsin; 1.
Pfam; PR00012; CHYMOTRYSIN.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00013; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000995; FN Type II; 1.
ProDom; PD000395; KrIngle; 1.
SMART; SM00181; EGF; 2.
SWART; SM00059; FN1; 1.
SWART; SM00059; FN2; 1.
SWART; SM00130; KR; 1.
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Best Local Similarity 32.5%
Matches 187; Conservative
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SEQUENCE 616
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34 SGAPCQRWT----VEATYRNWTEKQALSWGLGHHAFCRNPDNDTRPWCFV-WSGDRLSWD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 YCDVSACSAQDVA----YPEESPTE-PSTKLPGFDS-------CGKTEIAE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RK----IKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHCT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIK--TRHLKVVLGDQDLKKEEFHEQ-----SFRVEKIFKYSHYNERDEIPHND 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IALLKI-KPVDGHÇALESKYVKTVCLPDGSFPSGSE--CHISGWGVTETG--KGSRQLLD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDGT----YY 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 SINPCLNGGSCLLVEDHP-----LCRCPTGYTGYFCDLDLMATCYEGRGLSYRGQAGTTQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 NOHACLYWNSHLLLOENY-NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 YCGLEQCQTPTFAPLVVPESQESPSQAPSLSHAPNDSTDHQTSLSKTNTMGCGQ---RF
                                                                                                                                                                                                                                                                                                                                                              56 SSTLTHABUPDWYY---TEDQADPC-QPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKV
                                                                                                                                                                                                                                                                                                                                                                                                         QNTCKDNPCGRGQCLITQSPPYY-------RCVCK--HPYTGPSCSQVVPVC
                                                                                                                                                                                                                                                                                                                                                                                                                         155 RPNPCQNGATC---SRHKRRSKFTCACPDQFKGKFCEIGS-DDCYVGDGYSYRGKANRTV
                                                                                                                                                                                                                                                                                                                                                                              74 ATTENEDENOOMGYCLEPKKVKDHCSKHNPCHKGGTCINTENGPHCLCPEHLIGKHCQK-
     127;
                                                                                                                                                                                                                                                                                                                  Ouery Match
22.0%; Score 694; DB 11; Length 597;
Best Local Similarity 32.8%; Pred. No. 3.7e-55;
Matches 189; Conservative 69; Mismatches 191; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIKS 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptidase_S1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
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                                                                                                                                                                                                                                                                                 168 HKRRSKFTCACPDQFKGKFCEIGSDDCYVGDGYSYRGKMMRTVNQHACLYWNSHLLLQEN 227
                                                                                                                                              82 YTAQNPSAQALGLGKHNYCRNPDGDAKPWCHV-LKNRRLTWEYCDVPSCS------ 130
                                                                                                                                                                            PTEPSTKI.PGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHF- 346
                                                                                                                                                                                         131 -----TGGLRQYSQPQF-RIKGGLFADIASHPWQAAIFAKHE---ESPGERFL 174
                                                                                                                                                                                                                         347 CGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEBFHEQSFRVEKIFKYSHYNER 404
                                                                                                                                  228 YNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEES 287
                                                            3 SCRDE---KTQMIYQQHQSWLR-------PVLRSNRVEYCWCNSGRAQCSE 43
                                                                                                     293 SERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVC
                                           114 TCKDNPCGRGQCLITQSPPXYRCVCKHPYTGPSCSQVVPVCRPNP-----CQNG-ATCSR
                                                                                                                                                                                                                                                                                                                SROLLDAKVKLIANTLCNSROLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTC
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 25, Last annotation update)
Factor XII.
F12.
Whis musculus (Mouse).
Eukaryota, Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Euteleosia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 11 TaxID=10090;
                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 395
 EXDGTYYVYGIVSWGLECGKR - PGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                                                                                                                                      353 LNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNWR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                       597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
    Query Match
Best Local S:
Matches 162
                                                                                                                                                                                                                                                                                                                                                             216
                                                                                                                                                                               288
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29;

Gaps

132 154 178 210 269

345

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245

411 455

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412 IALLKI-KPVDGHCALESKYVKTVCLPDGSPPSGSE--CHISGWGVTETG--KGSRQLLD 466
                                                                                                                                                                                                                                                                                                                                                                                    RK----IKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTAAHCT 364
                                                                                                                                                                                                    RPNPCQNGATC---SRHKRRSKFTCACPDQFKGKFCEIGS-DDCYVGDGYSYRGKMRTV 210
                                                                           270 YCDVSACSAQDVA-----YPRESPTE-PSTKLPGFDS-------CGKTBIAE 308
                                                                                                                                                                                                                                                               :|||;| : | || : | : | || || || 456 LALLRLQESKTNSCALLSPHVQPVCLPSGAAPPSETVLCEVAGWGHQFEGAEEYBTFLQE
                                                                                                                                                                                                                                                                                                                                                                  467 AKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCBKDGT----YY
                                                                                                                                         365 DIK--TRHLKVVLGDQDLKKBEFHEQ-----SFRVEKIFKYSHYNBRDEIPHND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 NOHACLYWNSHLLLQENY-NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Oryctolagus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE 2155945; PubMed=12149463;
Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R., Dichek D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSMILD.
QSMILD.
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Urokinase-type plasminogen activator.
                                                                                                                                                                                                                                                                                                                                                                                                                               523 VYGIVŞWGLEÇĞKR.-PGVYTQVTKFLNWIKATIKŞ 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
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        155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 QNTCKDNPCGRGQCLITQSPPYY-------RCVCK--HPYTGPSCSQVVPVC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ATTPNFDEDQQWGYCLEPKKVKDHCSKHNPCHKGGTCINTPNGPHCLCPEHLTGKHCQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 SSTLTHAENPDWYY---TEDQADPC-QPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKV
                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch al Similarity 32.6%; Pred. No. 1.1e-54; 188; Conservative 70; Mismatches 191; Indels 127;
                                                                                                                                                                                                                 N SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVD/N; TISSUE=Liver;

A Strausberg R.; JAH49867; JAH49867.1; --

R SOLONGSSOB; CANTESCELLULAT; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

R GO; GO:0005509; F:Calcium ion binding; IEA.

R GO; GO:0005509; F:Calcium ion binding; IEA.

R GO; GO:0005509; F:Calcium ion binding; IEA.

R InterPro; IPRO0001; Cys Ser_trypsin.

R InterPro; IPRO0001; Cys Ser_trypsin.

R InterPro; IPRO0001; Cys Ser_trypsin.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R InterPro; IPRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R Pfam; PRO0001; Fibric.

R PRONTS; PRO0013; Fibric.

R PRONTS; SWOO013; Fibric.

R PROSITE; PSO00013; Fibric.

R PROSITE; PSO00013; Fibric.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPSIN.

R PROSITE; PSO00134; TRYPS
                                                       609 AA
                                                       PRT;
                                                       PRELIMINARY;
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Best Local S:
Matches 188
                                                       Q80YC5
                           RESULT 13
Q80YCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.2%; Score 667.5; DB 6; Length 433;
Best Local Similarity 37.2%; Pred. No. 6.8e-53;
Matches 155; Conservative 62; Mismatches 163; Indels 37; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 CQNGAICSRHKRRSK-FICACPDQFKGKFCEIGS-DDCYVGDGYSYRGKMRTVNQHACL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHISGWGVTETGK -- GSROLLDAKVKLIANTLCNSROLYDHMIDDSMICAGNLOKFGODT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 SAQDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 LIISMPQG----HFCGGALIHPCWVLTAAHC--TDIKTRHLKVVLGDQDLKKEEFHEQSF 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 RVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP----DGSFPSGSE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 EVEQLILHEGYSADTLAHHNDIALLKILSNNGQCAQPSRSIQTICLPPWNADPNF--GTS 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
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ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
BNART; SM00120; Tryp SPc; 1.
PROSITE; PS00022; EGF 1: 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS000134; TRYPSIN_DM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_BR; 1.
PROSITE; PS00135; TRYPSIN_BR; 1.
Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SEQUENCE 433 AA; 48375 MW; 65E64F36415549B0 CRC64;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
EMBL; AY029817; AAK40239.1; -.
EMBL; AB087224; BAC02685.1; -.
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01-001-2002 (TrEMBLrel. 22, Last sequence update)
01-001-2003 (TrEMBLrel. 25, Last annotation update)
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Q8MHY7
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277 SAQDVAYPEESPTEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLP 336
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GO; GO:001263; F:chymotrypsin activity; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:000823; F:peptidase activity; IEA.

RO; GO:006508; P:proteolysis and peptidolysis; IEA.

RICEPPO: IPRO00003; CAP. GET. LTYPSin.

RICEPPO: IPRO0001; KXINGle.

RICEPPO: IPRO01314; Peptidase 31.

RICEPPO: IPRO01314; Peptidase 51A.

RICEPPO: IPRO01314; Peptidase 51A.

RICEPPO: IPRO01314; FXINGle.

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21.1%; Score 666.5; DB 6; Length 4
Best Local Similarity 37.2%; Pred. No. 8.4e-53;
Matches 155; Conservative 61; Mismatches 164; Indels
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Job time : 41 secs
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Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 45, Appl	Sequence 1, Appliance Sequence 1, Appliance Sequence 6, Appliance 65, Ap	Sequence 53, Appl Sequence 67, Appl Sequence 61, Appl Sequence 4, Appli Sequence 8, Appli	Patent No. 5219569 Sequence 1, Appli Sequence 1, Appli	•				Gene Encoding Said Protein					Length 655; Indels 83; Gaps 21;
709.5 22.5 355 1 709.5 22.5 355 1 709.5 22.5 355 1 709.5 22.5 355 2	32 709.5 22.5 355 3 US-08-794 528-1 34 709.5 22.5 355 6 5223256-1 35 707.5 22.4 355 1 US-08-811-949-1 36 707.5 22.4 389 2 US-08-811-949-65 37 706.5 22.4 389 2 US-08-811-949-65	703.5 22.3 355 2 702.5 22.3 389 2 698 22.1 354 2 698 22.1 356 1 684 5 21.7 356 1	663 21.0 430 6 662.5 21.0 411 3 661.5 21.0 411 1		ALIGNMENTS	RESULT 1 US-08-148-910-12	; Sequence 12, Application US/08148910 ; Patent No. 5466593 ; GENERAL INFORMATION: APPLICANT: Takeni SHIMOWURA et al.	rotein and ck 1., #700	COMPUTER READABLE FORM: MEDIUM TYPE: 0.18 sketce 5.25 inch, MEDIUM TYPE: 0.18 sketce 5.25 inch,	COMPUTER: IBM Compatible COMPUTER: IBM Compatible COPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect	ο'	**PPLICATION NUMBER: US/UB/148,910 FILING DATE: No. 5466593ember 5, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: ATORNEY/AGENT INPORMATION: NAME: WARTEN M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 202-371-8856 TELECHONE: 100-371-8856 TELECHONE: 100-371-8856 TELECHONE: 100-371-8856 TENDENNES: 310-31 TYPE: amino acid STRANDENNES: aingle TOROLOGY: 1inear NOLECULE TYPE: protein US-08-148-910-12	Query Match 26.4%; Score 832.5; DB 1; Best Local Similarity 33.2%; Pred. No. 4e-53; Matches 192; Conservative 87; Mismatches 216;
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model Run on: May 24, 2004, 09:45:05; Search time 17:5 Seconds (without alignments) 1652.031 Million cell updates/sec	Title: US-09-912-559-3 Perfect score: 3154 Sequence: 1 MFARMSDLHVLLLMALVGKTTQVTKFLNWIKATIKSESGF 560	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 389414 segs, 51625971 residues	Total number of hits satisfying chosen parameters: 389414	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: Issued_Patents AA:* 1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:* 3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:* 4: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:* 5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Query	Descript	832.5 26.4 655 1 US-08-148-910-12 832.5 26.4 655 1 US-08-148-910-12 786 24.9 562 6 520913-1 767.5 24.3 527 2 US-08-181-949-39 77-15 24.3 527 2 US-08-181-949-39 766.5 24.3 527 1 US-08-181-949-39 766.5 24.3 527 6 US-08-811-949-39 766.5 24.3 527 6 US-08-811-949-43 766.5 24.3 562 2 US-08-811-949-43 766.5 24.3 562 2 US-08-83-795A-38 766.5 24.3 562 2 US-08-83-795A-38 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 766.5 24.3 562 6 5200340-2 720.2 22.3 477 2 US-08-811-949-49 772 22.9 437 2 US-08-811-949-49 772 22.9 546 6 5200340-6 775 5 22.7 78 4 US-08-811-949-55 775 5 22.7 78 4 US-08-811-949-55 775 775 775 775 775 775 775 775 775	/15.5 22.5 355 2 US-08-811-949-47 Sequenc 709.5 22.5 355 1 US-08-137-116-1 Sequenc 709.5 22.5 355 1 US-08-217-618-1 Sequenc

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 GGPAALDPCASGPCLNGGSCSNTQDPQSYHCSCPRAPTG-----KD--CGTEKCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA--QDVAYPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 RDEIPHNDIALLKLKPVDGHCALESKYVKTVCLPD--GSFPSGSECHISGWG-VTETGKG
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PATENT NO. 5244676

PATENT NO. 5244676

PATENT NO. 5244676

PATENT NO. 5244676

TOLUNAY, H.ESER, WARREN, THOMAS G.; WUN, TZE-CHEIN

TITLE OF INVENTION: MODIFIED TISSUE PLASMINGEN ACTIVATOR

WITH MODIFIED GLYCOSYLATION SITE

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

** APPLICATION NUMBER: US/07/203,047

** FILING DATE: 06-JUN-1988

SEQ ID NO:5:
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                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 4e-53;
7; Mismatches 216;
                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 33.2%; Pri
Matches 192; Conservative 87;
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                         12:
                                                                            INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERRISTICS: LENGTH: 655 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                           human
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288

308 406

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289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG 348
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             124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178
                                                                                                                                                                                                                                                       407 IPHNDIALLKIKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR
                                                                                                     229 NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP
                                                                                                                                                                            349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNERDE
                                               111 AECTINWIS----SALAQKPYSGR-----RPDAIRLGLGNHINYCRNPDRDSKPWCYV
                                                                                179 PDQFK-GKF-----CEIGSDDCYVGDGYSYRGROMRTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MOBERASHI, MASSKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 DGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-70x-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 39, Application US/08811949; Patent No. 5840533; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIWASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGDAKPWCHVLKNRRLTWEYCDVPSCSTCGLRQYSQPQF-RIKGGLFADIASHPWQAAIF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSLPLTISMPOGHFCGGALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKBEFHEQSF 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECH 448
                                                                                                                                                                                                                    NSHLLLQENYNMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA 278
                                                                                                                                                                                                                                                                                                                                                                         211 GNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNP 270
                                                                                                                                                                                                                                                                                                                                                                                                                ----PGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK--HRRSPGERFLÖGGILISSCWILSAAHÖPQERFPPHHLTVILGRTYRVVPGEREQKF 387
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                                                                                                                          112 ONTCKDNPCGRGOCLITOSPPYYR-----CVCKHPYTGPSCSQVVPV--CRPNPC
                                                                                                                                                             QVICRDE ---KTQMIYQQHQSWLRPVLRSNRVEYCWCN---SGRAQCHSVPVKSCSEPRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                   24.9%; Score 786; DB 6; Length 562;
33.8%; Pred. No. 8.5e-50;
ive 74; Mismatches 177; Indels 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5520913

Patent No. 5520913

PAPPLICANT: ANDERSON, STEPHEN, BENNETT, WILLIAM F., BOTSTEIN, DAVID, HIGGINS, DEBONRAH L., PACNI, NICHOLAS F., ZOLLER, WARK J. TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING; ZYMOGENIC PROPERTIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 35
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/88,451
FILING DATE: 06-UUL-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 770,510
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: 384,608
FILING DATE: 24-UL-1989
APPLICATION NUMBER: 24-UL-1989
FILING DATE: 02-SEP-1988
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Best Local Similarity 35.29
Matches 183; Conservative
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181; Conserv
; LENGTH: 562
5244676-5
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Best Local 8
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Matches
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214
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GENERAL INFORMATION:
APPLICANT: Generatech, Inc.
TITLE OF INVENTION: Specific Properties
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generach, Inc.
                                                                                                                                                                   85;
                                                                                                                                 Length 527;
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                                                                                                                               24.3%; Score 766.5; DB 1;
35.0%; Pred. No. 2.1e-48;
iive 77; Mismatches 176;
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COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy die

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: DAtin (Genemech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/01025A

FILING DATE: 19910214

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
527 amino acids
AMINO ACID
                                                                                                                                                                       Conservative
                      TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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PCT-US91-01025A-2
                                                                                ; MOLECULE TIP
US-07-609-510B-16
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Sequence 16. Application US/07609510B
Patent No. 5336700
GENERAL INFORMATION:
APPLICANT: Berge et al.
APPLICANT: Berge et al.
APPLICANTONS: Method for Altering Post-Translational Processing of Tissue CONESPONDENCE APPLESS: 16
NUMBER OF SEQUENCES: 16
NUMBER OF SEQUENCES: 16
STREET: Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
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ZIP: 46285

COMPUTER RADABLE FORM:
MEDIUM TYEE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILING DATE: 19901106
CLASSTRICATION: 435
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
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      527 amino acids
                                                                                                                                   al Similarity 35.0%
182; Conservative
                                                        , MOLECULE TYPE: protein US-08-811-949-39
                        amino acid
                                            linear
                    TYPE: amir
TOPOLOGY:
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STATE: II
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      LENGIH:
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US-08-811-949-43

US-08-811-949-43

i Sequence 43, Application US/08811949

i Patent No. 584051304

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SASALT, HITOSHI

APPLICANT: HAYASHI, MASAKO

ITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

ITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSE

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ADDRESSEE: TISS S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARRINGTON

CITY: ARRINGTON

TITLE OF TIVETON STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN STORMEN ST
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FILING DATE: 07-APR-1983

** APPLICATION UNDER: 398,003

FILING DATE: 14-UTL-1982

** APPLICATION NUMBER: 374,860

** FILING DATE: 05-MAY-1982

** LENGTH: 527
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.0%
Matches 182, Conservative
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STATE: VA
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 PDQFK-GKF-----CEIGSDDCYVGDGXSYRGKMNRTVNQHACLYWNSHLLLQENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY
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;Patent No. 5185259
; APPLICANT: GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA,
;VEHAR, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
;ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%; Score 766.5; DB 5;
35.0%; Pred. No. 2.1e-48;
tive 77; Mismatches 176;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/489,855
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12,694
FILING DATE: 09-FEB-1987
APPLICATION NUMBER: 483,052
                                                                                                    28,616
ER: 454P2
                   FILING DATE: 1 March 1990
ATTONEY AGENT INFORMATION:
NAME: Heask, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 454P2
TELECOMMUNICATION INFORMATION:
TELEFONE: 415/26-1896
TELEFONE: 415/952-9831
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
PCT-US91-01025A-2
     07/486,657
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 35.0%
Matches 182; Conservative
     APPLICATION NUMBER:
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407 IPHNDIALLKIKPVDGHCALBSKYVKTVCLP--DGSFPSGSECHISGWGVTBTGKG--SR 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAODVAYPEESP 288
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TAQNPSAQALGLGKHNYCRNPDGDAKPWCHV-LKNRRLTWEYCDVPSCS------ 297
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: 08LON, NORMAN F.
NAME: 08LON, NORMAN F.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 703-413-3200
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.3%; Score 766.5; DB 2; Best Local Similarity 35.0%; Pred. No. 2.3e-48; Matches 182; Conservative 77; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-811-949-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463
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LENGTH: 562 amino acids TYPE: amino acid STRANDEDNESS: single

linear

OPERATURE SYSTEM: FC-LOS/MS-LOS
SOFTWARE: PACEDIA #1.00 Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION NUMBER: P4 40 892.7
FILING DATE: 17-NOV-1994
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNYA ARENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 148/42448
TELECONMUNICATION INFORMATION:
TELECONMUNICATION INFORMATION:
TELEFAX: (202) 628-8800
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804
TELEFAX: (202) 628-8804

ZIP: 2005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relace

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, EC
STREET: 1200 G Street, N.W., St
CITY: Washington
STATE: DC
COUNTRY: USA

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229 NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP 288
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                                                                                                                                       86 CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDIRATCYEDQGISYRGTWSTAESG
                                                                                                                                                                                    124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC
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                                                                             85;
                                                                                                                    77 COPNECEHGGDC--LVHGSTFTCSCLAPFSGNKCO-KVONTCKDNP--CGRG-
                                                                                 Indels
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                                                  Query Match 24.3%; Score 766.5; DB 2; Best Local Similarity 35.0%; Pred. No. 2.3e-48; Matches 182; Conservative 77; Mismatches 176;
, MOLECULE TYPE: protein US-08-560-098A-50
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GENERAL INFORMATION:
APPLICANT: WNENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: APPERENCY
APPLICANT: PRINCE OF THE STEPHENS, See A JOSE
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties

RESULT 10 US-08-560-098A-50 ; Sequence 50, Application US/08560098A ; Patent No. 5976841

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-OCLITOSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178
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107 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR 462
                                                                                                                          462 RLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLN
                                                                                                                                                                                                                                                                                                                                        % Sequence 4, Application US/09703695A

| Sequence 4, Application US/09703695A
| Patent No. 6533097
| GENERAL INFORMATION:
| APPLICANT: Xu, Yuan
| TITLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
| FILE REPERENCE: P1788R1
| CURRENT APPLICATION NUMBER: US/09/703,695A
| CURRENT APPLICATION NUMBER: US/09/703,695A
| PRIOR FILING DATE: 1999-11-04
| WINDER OF SEQ ID NOS: 4
| SEQ ID NO 4
| LENGTH: 562
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                                 402 TYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSE
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                                                                                           QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTCBK
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                                                                                                                                                                                        DGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
24.3%; Score 766.5; DB 4;
Best Local Similarity 35.0%; Pred. No. 2.3e-48;
Matches 182; Conservative 77; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-703-695A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                   RESULT 11
US-08-803-795A-38
Sequence 38 Application US/08883795A
Sequence 38 Application US/08883795A
Sequence 38 Application US/08883795A
Sequence 38 Application US/08883795A
Sequence 38 Application US/08883795A
SEQUENCE 38 APPLICANT: Awang, Genevieve
APPLICANT: Awang, Genevieve
APPLICANT: Awang, Genevieve
APPLICANT: Awang, Genevieve
APPLICANT: ADDRESS:
ADDRESSE: BERESKIN & PARR
STREET: 40 King Street West
CTITY: Toronto
STATE: Ontario
COMPUTER: End Street West
CTIPY: Toronto
STATE: Ontario
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-1UN-1997
CLASSIFICATION: 435
ATTOMEY/AGENT INPORMATION:
APPLICATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 41,394
INPORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
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     DGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein (tPA)
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$Patent No. 5344773

$Patent No. 5344773

$Patent No. 5344773

$1 APPIICANT: ALLAW, DOUGLAS, RICHARD, LENONTT, JEPREY F.; DACKOWSKI, WILLIAW, DOUGLAS, RICHARD, COLE, EDWARD S.; PURCELL JR., RICHARD D.; LAU, DAVID TAI-YUI TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN ACURERY PROJUCED BY RECOMBIANT DNA

**ACTIVATOR PROJUCES: 6

CURRENT APPLICATION DATA:

**PRING DATE: 01-0CT-1985

**PRING DATE: 01-0CT-1984

**FILING DATE: 01-0CT-1984
                                                                                                          Query Match 24.3%; Score 766.5; DB 6; Best Local Similarity 35.0%; Pred. No. 2.3e-48; Matches 182; Conservative 77; Mismatches 176;
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
                                              ;SEQ ID NO:2:
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1 LENGTH: 562
5200340-2
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TAQNPSAQALGLGKHNYCRNPDGDAKPWCHV-LKNRRLTWEYCDVPSCS------
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   ; Patent No. 5185259
; Patent No. 5185259
; VEHAR, GOEDDEL, DAVID V.;KOHR, WILLIAM J.;PENNICA,
;VEHAR, GORDON A.
; TILLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
;ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 DGTYYVYGIVSWGLECGKR--PGVYTQVTKFLNWIKATIK 555
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                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATE:

APPLICATION DATE: 12,694

FILING DATE: 09-FEB-1987

APPLICATION NUMBER: 12,694

FILING DATE: 09-FEB-1987

APPLICATION NUMBER: 398,003

FILING DATE: 14-UL-1982

APPLICATION NUMBER: 374,660

FILING DATE: 05-MAY-1982
                                                                                                                                                                                                                                                                                                                            SEQ ID NO:3:
LENGTH: 562
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146 AECTIWANS----SALAQKPYSGR------RPDAIRLGLGNHNYCRNPDRDSKFWCYV 192

124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRKFTCAC

86

77 COPNECEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP--CGRG--

85;

Indels

193 ---FKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY

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179

NMFWEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP 289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG

229 250 406

298 -----TCGLRQYSQPQF-RIKGGLFADIASHPWQAAIFAK--HRRSPGERFLCG 349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEBFHEQSFRVEKIFKYSHYNERDE 463 QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTCEK 517

402

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518

407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR

343

462

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85;
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                                         Query Match 24.3%; Score 766.5; DB 6; Length Best Local Similarity 35.0%; Pred. No. 2.3e-48; Matches 182; Conservative 77; Mismatches 176; Indels
5344773-2
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PACION NO. 5200340

PAPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.;O'HARA,;PARICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
TILLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN;ACTIVATORS
NUMBER OF SEQUENCES: 34

5200340-2

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463 QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QPTCQGDSGGPLTCEK 517
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298 ------TCGLRQYSQPQF-RIKGGLFADIASHPWQAAIFAK--HRRSPGERFLCG 343
                                                                                                                                                                                                                                                                  349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHBQSFRVBKIFKYSHYNBRDB 406
                                                                                                                                                                                                                                                                                      407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTFTGKG--SR 462
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                                                                                                                                               229 NWFWEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP 288
86 CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYRGTWSTAESG 145
                            124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178
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Search completed: May 24, 2004, 09:50:30 Job time : 19.5 secs

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Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Database :

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Sequence 3, Application US/09912559
; Sequence 3, Application US/09912559
; Patent No. US20020142316A1
GENERAL INFORMATION:
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: ROEMISCH, HANS-ARNOLD
APPLICANT: BLANG, WIEGAND
APPLICANT: BLANG, WIEGAND
APPLICANT: BLANG, WIEGAND
APPLICANT: BLANG, WIEGAND
APPLICANT: WEINER, THOMAS
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14 US-10-193-656-8
16 US-10-443-011-4
15 US-10-410-962-26
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18 US-10-449-132-2
19 US-10-172-712-30
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10 US-09-987-414
10 US-10-111-085-11
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ORGANISM: Homo sapiens
US-09-912-559-3
              Query Match
Best Local Simi
Matches 560;
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1: \cgn2_6\prodata/1\pubpaa/US07_PUBCOMB.pep:*

2: \cgn2_6\prodata/1\pubpaa/PCT_TRW_PUBLPEpp:*

2: \cgn2_6\prodata/1\pubpaa/US07_NEW_PUBLPEpp:*

4: \cgn2_6\prodata/1\pubpaa/US06_NEW_PUB.pep:*

5: \cgn2_6\prodata/1\pubpaa/US06_PUBCOMB.pep:*

6: \cgn2_6\prodata/1\pubpaa/US07_NEW_PUB.pep:*

7: \cgn2_6\prodata/1\pubpaa/US08_NEW_PUB.pep:*

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17: \cgn2_6\prodata/1\pubpaa/US08_PUBCOMB.pep:*

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1 MFARMSDLHVLLIAMALVGKT......TQVTKFLNWIKATIKSESGF
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                                     GenCore version 5.1.6
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US-09-997-455-18

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Maximum Match 100%
Listing first 45 summaries
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MFARMSDLHVLLLMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT
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                  RESULT 2

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10SENERAL INFORMATION:
1 APPLICANT: GRIFFIN, JOHN H.
1 APPLICANT: GRIFFIN, JOHN H.
2 APPLICANT: GRIFFIN, JOHN H.
3 APPLICANT: BELLEGUER, JEAN-LUC
1 APPLICANT: PELLEGUER, JEAN-LUC
2 TITLE OF INVERTION: STABLIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS
1 TITLE OF INVERTION: STABLIZED PROTEINS WITH ENGINEERED DISULFIDE BONDS
1 TITLE OF INVERTION WIMBER: US/10/172,712

1 CURRENT PILING DATE: 2001-09-30

1 PRIOR APPLICATION NUMBER: 6/298,578

1 PRIOR APPLICATION NUMBER: 6/298,578

1 SEQIED NOS: 32

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1 TYPE: PRI
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Best Local Similarity 100.0%; Pred. No. 9.1e-241;
Matches 560; Conservative 0; Mismatches 0; Indels 0;
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US-10-172-712-32
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GENERAL INFORMATICAN
APPLICANT KIECHL, STEFAN
APPLICANT WIEDERT, JOHANN
APPLICANT WIEDERMANN, CHRISTIAN JOSEF
APPLICANT WIEDERMANN, CHRISTIAN JOSEF
APPLICANT BOOKINGT, JUERGEN
APPLICANT FEUSANER, ANNOLE
APPLICANT FEUSANER, ANNOLE
APPLICANT STORER, HANS-ARNOLD
APPLICANT STORER, HANS-ARNOLD
APPLICANT STORER, HANS-ARNOLD
APPLICANT STORER, HANS-ARNOLD
APPLICANT STORER, HANS-ARNOLD
APPLICANT STORER, 1457-01
TITLE OF INVENTION: (FSAP) AS RISK FACTOR VII ACTIVATING PROTEASE
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
CURRENT FILING DATE: 2003-03-19
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR APPLICATION NUMBER: DE 100 50 40.4
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR APPLICATION NUMBER: DE 101 18 706.8
PRIOR APPLICATION NUMBER: DE 101 18 706.8
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PRIOR PRIOR PLING DATE: 2001-04-12
SEQUENCE TYPE: PRIOR FILING DATE: 2001-04-12
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APPLICANT: WILLELY JOHANN
APPLICANT: WEINER, THOMAS
APPLICANT: FEUSNER, ANNETE
APPLICANT: FEUSNER, ANNETE
APPLICANT: STORHK, HAN SANOLD
APPLICANT: STORHK, HAN SANOLD
APPLICANT: STORHK, HAN SANOLD
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APPLICANT: STORHK, HAN SANOLD
APPLICANT: STORHK, HAN SANOLD
APPLICANT: STORHK APPLICATION WARBURG IN WITANT OF FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (SAP) 110/391,215
CURRENT FILING DATE: 2003-03-19
PRIOR APPLICATION NUMBER: 09/912,559
PRIOR APPLICATION NUMBER: DE 100 36 641.4
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Pred, No. 1.6e-240;
1; Mismatches 0;
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Publication No. US20040009543A1
GENERAL INFORMATION:
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; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 7; LENGTH: 560
                                                                                                                                                   Query Match
Best Local Similarity 99.8
Matches 559; Conservative
                                              LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-391-215-7
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APPLICANT: WILLEIT, JOHANN
APPLICANT: WILLEIT, JOHANN
APPLICANT: WILLEIT, JOHANN
APPLICANT: WIELERMANN, CHRISTIAN JOSEP
APPLICANT: WIELERMANN, CHRISTIAN JOSEP
APPLICANT: PEUGSHAN, UDERGEN
APPLICANT: FEUGSHER, HANS-ARNLID
APPLICANT: FEUGSHER, HANS-ARNLID
APPLICANT: FORESAM, VOLKER
APPLICANT: STOEHR, HANS-ARNLID
APPLICANT: ODERSAM, VOLKER
TITLE OF INVENTION: MARSHER INSTANCE FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: MARSER: US/10/391,215
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: DE 100 52 319.6
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
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PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2001-04-12
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                             Gaps
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                           Indels
      Pred. No. 9.1e-241;
Mismatches 0;
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         Best Local Similarity 100.0%; P
Matches 560; Conservative 0;
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99.6%; Pred. No. 6.7e-240;
iive 1; Mismatches 1;
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Best Local Similarity 99.6
Matches 558; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-559-4
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Pred. No. 3.9e-240;
0; Mismatches 1;
           PRIOR FILING DATE: 2000-07-26

PRIOR APPLICATION WUNBER: DE 100 50 040.4

PRIOR PLILING DATE: 2000-10-10

PRIOR PLILING DATE: 2000-10-21

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 560

TYPE: PAT

ORGANISM: Homo sapiens

US-10-391-215-6
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Patent No. US20020142316A1
GENERAL INFORMATION:
APPLICANT: ROEMISCH, UUERGEN
APPLICANT: STOEHR, HANS-ARNOLD
APPLICANT: LANG, WIEGAND
APPLICANT: HEUSNERF, ANNETTE
APPLICANT: HEUSNERF, ANNETTE
APPLICANT: WEIGHN
APPLICANT: WEIGHN
APPLICANT: WEIGHN
APPLICANT: NERLICH, CLAUDIA
APPLICANT: MAUTH-NAUMANN, GUDRUN
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.8%;
Matches 559; Conservative
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US-09-912-559-4
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APPLICANT: WIEDERMANN, CHRISTIAN JOSEF
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: THOMAS.
APPLICANT: PUESANER, ANNETTE
APPLICANT: STOEHR, HANS-ARNOLD
APPLICANT: DOERSAN, VOLKER
TITLE OF INVENTION: MARBURG I MUTANT OF FACTOR VII ACTIVATING PROTEASE
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS
CURRENT APPLICATION NUMBER: US/10/391,215
PRIOR FILING DATE: 2000-0-26
PRIOR FILING DATE: 2000-0-26
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 100 50 400-4
PRIOR FILING DATE: 2000-10-21
PRIOR PILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR PELING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VOS: 8
LENGTH: 560
TYPE: PRI
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CRGANISM: Homo sapiens
US-10-391-215-8
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229 NMFMEDAETHGIGBENFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA--QDVAYPEE 286
321 VDSVQAAALLGLGPHAYCRNPDNDERPWCYV-VKDSALSWEYCRLEACESLTRVQLSFDL 379 155 228 261 ATGITVCACPPGFAGRLCNIEPDERCFLGNGTGYRGVASISASGLSCLAWNSDLLYQELH 320 SPTEPSTKLPGFDSCGKTEIAERKIK-RIYGGFKSTAGKHPWQASLQSSLPLTISMPQGH 345 FCGGALIHPCWVLTAAHCTDIKTRH--LKVVLGDQDLKKEEFHEQSFRVEKIFKYSHYNE 403 608 203 127 ITQSPPYY------RCVCKHPYIGPSCSQVV--PVCRPNPCQNGATCSRHK 169 204 DETRYEYLEGGDRWARVRQGHVEQCEC---FGGRTWCEGTRHTACLSSPCLNGGTCHLIV 170 RRSKFTCACPDQFKGKFCEIGSDD-CYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY 380 LAİLPEPASPGRQACGRRHKKRIFLRPRİLGGSSLPGSHPWLAAIYIG-----DS 156 GGPAALDPCASGPCLNGGSCSNTQDPQSYHCSCPRAFTG------KD--CGTEKCF 461 -SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQDTCQGDSGGPLTCEKDG -----DPCQPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPCGRGQCL DISULFIDE BONDS 31 ESLDPDWTPDQYDYSYEDYNQEENTSSTLTHAENPDW-----YYTEDQA----US-10-172-712-28

US-10-172-712-28

| Sequence 28, Application US/10172712
| Sequence 28, Application US/10172712
| Publication No. US20030125232A1
| GENERAL INFORMATION:
| APPLICANT: GRIFFIN, JOHN H.
| APPLICANT: GRIFFIN, JOHN H.
| APPLICANT: GRIFFIN, JOHN H.
| APPLICANT: GRIFFIN, JOHN H.
| APPLICANT: GRIFFINGEN, JEN-LUC
| TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISU
| FILE REFERENCE: 4198-4001US1
| CURRENT FILING DATE: 2002-09-30
| PRIOR PALICATION NUMBER: 60/298,578
| PRIOR PLILING DATE: 2001-06-14
| NUMBER OF SEQ. ID NOS: 32
| SOFTWARE: Patentin Ver. 2.1
| SEQ. ID NO 280 DB 14; Length Indels |:|||:||| ||: :|||||| ||: 646 TYYVYGIVSWGLECGK--RPGVYTQVTKFLNWIKATIK 555 26.4%; Score 832.5; DB 14; 33.2%; Pred. No. 3.9e-57; iive 87; Mismatches 216; RESULT 9 US-09-374-298-145 'Sequence 145, Application US/09974298 'Patent No. US20020156263A1 Query Match Best Local Similarity 33.2%; Matches 192; Conservative TYPE: PRT
CORGANISM: Homo sapiens
US-10-172-712-28

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APPLICANT: Manosroi, Jiradej
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatian
APPLICANT: Tayapiwatian
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REPERENCE: 0652.2180001
CURRENT APPLICATION NUMBER: US/09/987,457
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                                                                                                                                                                                                                    SEATURE:
NAME/KEY: misc_feature
CTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
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TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REPERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                              Query Match
24.3%; Score 767.5; DB 9;
Best Local Similarity 35.0%; Pred. No. 4.4e-52;
Matches 182; Conservative 77; Mismatches 176;
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Publication No. US20030013150Al
GENERAL INFORMATION:
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                       ; OTHER INFORMA
US-09-974-298-145
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US-09-987-457-18
                                                                                                                                                 SEQ ID NO 145
LENGTH: 562
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APPLICANT: Aranya Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
TITLE OF INVENTION: Methods for Large Scale Production
TITLE OF INVENTION: NA-Desived tPA or K2S Molecules
TITLE OF INVENTION: 10/09/997,455
CURRENT FILING NATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,574
PRIOR PILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-02-15
PRIOR FILING DATE: 2001-11-14
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35.0%; Pred. No. 4.9e-52;
tive 77; Mismatches 176;
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/268,573
PRIOR FILING DATE: 2000.02-15
PRIOR APPLICATION NUMBER: GB 00 27 782.
PRIOR PILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 18
LENGTH: 527
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; Sequence 19, Application US/09987455
; Publication No. US20030049729A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
; ORGANISM: Homo sapiens (tPA)
US-09-987-457-18
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Best Local Similarity 35.04
Matches 182; Conservative
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Best Loca
Matches
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                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                       Length 527;
                                                                                                                                                                                                                                 tch 24.3%; Score 766.5; DB 10; Length al Similarity 35.0%; Pred. No. 4.9e-52; 182; Conservative 77; Mismatches 176; Indels
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Veronica A. CARROLL
APPLICANT: Adrian L. HARRIS
APPLICANT: ROY BICKNELL
APPLICANT: Pat PRICE
TITLE OF INVENTION: MODULATION OF CELL GROWTH
FILE REFERENCE: 117-450 / N.75907A SER
CURRENT PAPLICATION NUMBER: US/10/432,842
CURRENT FILING DATE: 2003-09-27
PRIOR PELICATION NUMBER: PCT/GE01/05244
PRIOR APPLICATION NUMBER: PCT/GE01/05244
PRIOR APPLICATION NUMBER: CB 0029001.5
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: MS WORD
SEQ ID NO 1
LENGTH: 527
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 527
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CRGANISM: Homo sapiens
US-10-432-842-1
                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-09-987-455-19
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US-10-432-842-1
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Best Local S:
Matches 182
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Sequence 203, Application US/10360101
Publication No. US20040009550A1
GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
TITLE OF INVENTION NUMBER: US/10/360,101
CURRENT APPLICATION NUMBER: US/2007060.8
FRIOR PAPLICATION NUMBER: US/2007060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 203
LENGTH: 527
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                                                                                                                                                                                                      111 ABCTNWNS----SALAQKPYSGR------RPDAIRLGLGMHNYCRNPDRDSKPWCYV 157
                                                                                                                                                                                                                                                179 PDOFK-GKF-----CEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY 228
                                                                                                                                                                                                                                                                                                                                   229 NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP 288
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                                                                                                          -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC
                                                                                                                                                                                                                                                                                      158 ---PKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY
                                                                                77 CQPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP--CGRG-----
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Query Match
24.3%; Score 766.5; DB 12; Length
Best Local Similarity 35.0%; Pred. No. 4.9e-52;
Matches 182; Conservative 77; Mismatches 176; Indels
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ORGANISM: Artificial Sequence
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US-10-360-101-203
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		RESULT 15 US-10-411-037-26 ; Sequence 26, Application US/10411037 ; Publication No. US20040043446A1 ; GENEAL INFORMATION ; APPLICANT: Neose Technologies, Inc. ; APPLICANT: DeFrees, Shawn ; APPLICANT: Bayer, Robert ; APPLICANT: APPLICANT: Applicant: Hakes, David	AFFLICANT: Bowe, Caryn TITLE OF INVENTION: ALEPA GLACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA TITLE OF INVENTION: GLACTOSIDASE A FILE REFERENCE: 040853-01-5082 CURRENT APPLICATION NUMBER: US/10/411,037 CURRENT FILING DATE: 2003-04-09 FRIOR PILING DATE: 2001-10-19 FRIOR PILING DATE: 2001-10-19 FRIOR PILING DATE: 2001-10-19 FRIOR PILING DATE: 2002-06-07 FRIOR PILING DATE: 2002-06-07 FRIOR PILING DATE: 2002-06-07 FRIOR PILING DATE: 2002-06-07 FRIOR PILING DATE: 2002-06-07 FRIOR PILING DATE: 2002-06-07 FRIOR APPLICATION NUMBER: US 60/391,777 FRIOR APPLICATION NUMBER: US 60/391,777 FRIOR APPLICATION NUMBER: US 60/404,249 FRIOR APPLICATION NUMBER: US 60/404,249 FRIOR FILING DATE: 2002-08-16 FRIOR FILING DATE: 2002-08-16 FRIOR FILING DATE: 2002-08-16 FRIOR FILING DATE: 2002-08-16 FRIOR FILING DATE: 2002-08-16 FRIOR SPLING DATE: 2002-08-16 FRIOR FILING DATE: 2002-08-16	y EDG TH NO 26 y EDG TH: 562 y TYPE: PRT y ORGANISM: Homo sapiens y ORGANISM: Homo sapiens Query Match Best Local Similarity 35.0%; Pred. No. 5.3e-52; Matches 182; Conservative 77; Mismatches 176; Indels 85; Gaps 20; An TOCONFOCHICGOL-LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP-CGRG 123 Qy 77 COPNFCEHGGDCLVHGSTFYCSCLAPFSGNKCQ-KVQNTCKDNP-CGRG
OY 124 -QCLITQSPEYYRCVCKHPYTGPSCSQVVPVGRENPCQNGATGSRHKRREKFTGAC 178 11 AECTNWANSSALAQKPYSGR	289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG 348 :	TYDNDIALLAUKSDESSENATURE TO SEE SELECTION OF TYDNDIALLOUKSDESSENATURE TYDNDIALLOUKSDESSENATURE TYDNDIALLOUKSDESSENATURE TYDNDIALLOUKSDESSENATURE TYDNDIALLOUKSDESSENATURE TYDNDIALLOUKSPENESSENATURE TYDNALCAGDIRSGGPQANLHDACQGDSGGPLYCLN BIRKEAHYRLYPSSENCTSCHILNRTYTONALCAGDIRSGGPQANLHDACQGDSGGPLYCLN DGTYYYYGINSWGLEGGRE - PGVYTCYTKFLNWIKATIK 555	JLT 14 99-969-271-7 Squence 7, Application US/099 squence 7, Application US/099 APPLICANT: Pfizer Inc. (All d APPLICANT: Pfizer Limited (G IITLE OF INVENTION: Pharmaceu FILE REFERENCE: PCS10951APME FILE OF INVENTION PHARMER: UCRRENT APPLICATION NUMBER: QB PRIOR PLILING DATE: 2000-10-17 NUMBER OF SEQ ID NOS: 7 LENGTH: 562 SQUENCH: 562 LENGTH: 562 CALLO NOS: 7 LENGTH: 562 CALLO NOS: 7 LENGTH: 562 CALLO NOS: 7 LENGTH: 562 CALLO NOS: 7 LENGTH: 562 LENGTH: 563 LEN	Best Local Similarity 35.0%; Pred. No. 5.38-52; Matches 182; Conservative 77; Mismatches 176; Indels 85; Gaps 20; Qy

	GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - pr	OM protein - protein search, using sw model
Run on:	May 24, 2004, 09:39:54 ; Search time 54 Seconds (without alignments) 2930.122 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-912-559-4 3153 1 MFARMSDLHVLLLMALVGKTTQVTKFLNWIKATIKSESGF 560
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	1586107 segs, 282547505 residues
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: geneseqp1980s:*
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ALIGNMENTS

Human blood coagulation factor VII activating protease mutant.

Human; blood coagulation factor VII activating protease; FSAP; single-chain plasminogen activator; bleeding disorder; haematological; haemostatic; mutant; mutein.

Weimer T, Becker M; Roemisch J, Stoehr H, Feussner A, Lang W, Nerlich C, Muth-Naumann G; New nucleic acid encoding mutant factor 7 activating protease, useful for diagnosis, treatment and prevention of coagulation disorders, also related protein and antibodies.

Disclosure; Page 20-22; 27pp; German.

The present invention relates to a mutant of the DNA sequence encoding the protease (FSAP) that activates blood coagulation factor VII (FVII) and single-chain plasminogen activator, where at least one of the base changes G to C at nucleotide 1177 and G to A at nucleotide 1601 is present. The mutant sequences can be used in the treatment and prevention of bleeding disorders associated with inherited or acquired defects of

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blood coagulation factors V, VIII, IX, X, XI, XII, von Willebrand's factor and/or with antibodies against any of these proteins. The present sequence is the mutant human FSAP protein
                                                                                                                                                                                                                                                                                                                                                            GRGQCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPD
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                                                                                                                                                                                        1 MFARMSDLHVLLLMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT
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                                                                                                              Length 560;
                                                                                                            100.0%; Score 3153; DB 5; Length
100.0%; Pred. No. 7.5e-186;
tive 0; Mismatches 0; Indels
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Human; open reading frame, ORFX, detection, cytostatic, hepatotropic, vulnerary; antipsoriatic, antiparkinsonian; noctropic, neuroprotective; anticonvulsant; osteopathic; antiparkintic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antifungal; antifrenmatic; antichyroid; antiantanemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; proliferative disorder; hypertension; cardiavascular disease; dabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuxia; burn; wound;
RESULT 2
AAB42484
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61 HAENPDWYYTEDQADPCQFNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC 120

61 HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPPSGNKCQKVQNTCKDNPC 121 GRGQCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPD

1 MFARMSDLHVLLLIMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT

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1; Indels

99.7%; Score 3143; DB 3; 99.6%; Pred. No. 3.1e-185; tive 1; Mismatches 1;

558; Conservative

Similarity

Query Match

Length 560;

1 MFARMSDLHVLLLMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT

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121 GRGQCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQNGATCSRHKRRSKFTCACPD 180

181 QFKGKFCEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGI 181 QFKGKFCEIGSDDCYVGDGYSYRGKANRIVNQHACLYMNSHLLLQENYNMFWEDAETHGI 241 GEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDS 300

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; heptotropic; vulnerary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; osteopathic; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; osteopathic; cardiant; thrombolytic; coagulant; vasofropic; antibateic; hypotensive; dermatological; immunosuppressave; antiinflammatory; antibacterial; antifungal; antitheumanic; antibyroid; and antianaemic. The activiral; antifungal; antitheumanic; antibyroid; and antianaemic. The cogness on pe used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OKFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, disorders, osteoarthritis, graft vs host disease, cardiovascular disease, (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, and as a contraceptive enhance coagulation; to inhibit thrombosis, and as a contraceptive
damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 3681-3683; 5507pp; English
                                                                                                                                                                                                                                      99US-0127607P.
99US-0127636P.
99US-0127728P.
                                                                                                                                                                                                31-MAR-2000; 2000WO-US008621.
                                                                                                                                                                                                                                                                                                        30-MAR-2000; 2000US-00540763
                         thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC76693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 560 AA;
                                                                                                            MO200058473-A2.
                                                                    Homo sapiens.
                                                                                                                                                                                                                                           31-MAR-1999;
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05-APR-1999;
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Length 560;
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                                                                                               Score 3143; DB 5;
Pred. No. 3.1e-185;
1; Mismatches 1;
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sequence is the human FSAP protein
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                                                                                                     Query Match
Best Local Similarity 99.6%;
Matches 558; Conservative
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(first entry)
                                                      Sequence 560 AA;
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20-NOV-1992;
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06-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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     GEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESPTEPSTKLPGFDS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; blood coagulation factor VII activating protease; FSAP; single-chain plasminogen activator; bleeding disorder; haematological; haemostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding mutant factor 7 activating protease, useful diagnosis, treatment and prevention of coagulation disorders, also related protein and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                        CGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA
                                                                                                                                                                                    AHCTDIKTRHIKYVIGDODIKKEEFHEQSFRVQKIFKYSHYNERDEIPHNDIALIKIKPV
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Muth-Naumann G;
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10-0CT-2000; 2000DE-01050040.
21-0CT-2000; 2000DE-01052319.
12-APR-2001; 2001DE-01018706.
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N-PSDB; AAL45696.
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Nerlich C,
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                                                                                                              HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC 120
                                                                                                                                             61 HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFGGNKCQKVQNTCKDNPC 120
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                                                                                                                                                                                                                                                                                          361 AHCTDIKTRHLKVVLGDQDLKKEEFHEQSFRVQKIFKYSHYNERDEIPHNDIALLKLKPV
                                    1 MFARMSDLHVLLLMALVGXTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT
                                                         1 MFARMSDLHVILLMALVGKTACGFSLMSLLESLDPDWTPDQXDYSYEDYNQEENTSSTLT
  Gaps
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(first entry)

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JP08027026-A
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                                                               Homo sapiens
08-AUG-1996
                                                                                                                                30-JAN-1996
                                      liver; huma hepatitis.
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e two chain HGF from inactive single
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                                                                                                                                                                                                                           RWARVROCHVEO-----CEC---FGGRTWCEGTRHTACLSSPCLNGGTCHLIVATGTTV
                                                                                                                                                                                                                                                                                                                 CACPDQFKGKFCEIGSDD-CYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQBNYNMFMED
                                                                                                                                                                                                                                                                                                                           AETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA--QDVAYPEESPTEPS
                                                                                                                                                                                                                                                                                                                                                                                 TKLPGFDSCGKTEIAERKIK-RIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGAL
                                                                                                                                                                                                                                                                                                                                                                                               PASPGRQACGRRHKKRTFLRPRIIGGSSSLPGSHPWLAAIYIG-----DSFCAGSL
                                                                                                                                                                                                                                                                                                                                                                                                                 IHPCWVLTAAHCTDIKTRH--LKVVLGDQDLKKEEFHEQSFRVQKIFKYSHYNERDBIPH
                                                                                                                                                                                                                                                 -----DPCQPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKC--QKVQNTCK----D
                                                                                                                                                                                                                                                                GGPAALDPCASGPCLNGGSCSNTQDPQSYHCSCPRAFTGKDCGTBKCFDETRYEYLEGGD
                                                                                                                                                                                                                                                                                NPCGRGQCLITQSPPYYRCVCKHPYTGPSCSQVV--PVCRPNPCQNGATCSRHKRRSKFT
                                                                                                                        Hepatocyte growth factor converting protease is capable of converting inactive single chain hepatocyte growth factor (HGF) into active two chain HGF by cleavage at a specific site. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                Length 655;
                                 Miyazawa
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                                                                                                                                                                                 Score 822.5; DB 2;
Pred. No. 1.6e-42;
); Mismatches 221;
                                 Kitamura
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                                                                         Hepatocyte growth factor converting pencoding them - for producing active
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                                                                                                          12; Page 21-24; 30pp; English
                                 Morimoto
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33.2%; Pre
cive 90;
                 (MITU ) MITSUBISHI KASEI CORP
 92JP-00312242
                                                                                                                                                                                                   Conservative
                                 자,
                                 Yamada
                                                WPI; 1994-152921/19.
N-PSDB; AAQ63951.
                                                                                                                                                                                          Similarity
                                                                                                                                                                  Sequence 655 AA;
 20-NOV-1992;
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                                                                                  encoding t
chain HGF.
                                  Shimomura
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standard; protein; 655

AAR89197

RESULT 5
AAR89197
ID AAR8
XX
AC AAR8

AAR89197,

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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 ITOSPPYY------RCVCKHPYTGPSCSOVV--PVCRPNPCQNGATCSRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 DETRYBYLEGGDRWARVROGHVEQCEC---FGGRTWCEGTRHTACLSSPCLNGGTCHLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 ATGTTVCACPPGFAGRLCNIEPDERCFLGNGTGYRGVASTSASGLSCLAWNSDLLYQELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSA--QDVAYPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPTEPSTKLPGFDSCGKTEIAERKIK-RIYGGFKSTAGKHPWQASLQSSLPLTISMPQGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 QALTEDGRPCRFPFRYGGRMLHACTSEGSAHRK---WCATTHNYDRDRAWGYCVEATPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DECOPNECEHGGDC---LVHGSTFTCSCLAPFSGNKCOKVQNTCKDNPCGRGQCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRSKFTCACPDQFKGKFCEIGSDD-CYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY
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                                     , single chain; hepatocellular growth factor; dimerisation; double chain; serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.9e-42;
3; Mismatches 217;
hepatocellular growth factor single chain
                                                                                                                                                                                               356. .655
/note= "mature peptide"
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 6-8; 8pp; Japanese.
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32.9%; Pre
tive 88;
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Best Local Similarity 32.99
                                              inactive;
                                              Mature protein; inactive;
liver; human; precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (MITU ) MITSUBISHI CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New preventative and useful for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-136206/14.
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193 ---FKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY 249
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                                                                                                                                                                                                                                                                                                                                 263 -----TCGLRQXSQPQF-RIKGGLFADIASHPWQAAIFAK--HRRSPGBRFLCG 308
                                                                                                                                                                                                                                                                                                                                                                                             349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVQKIFKYSHYNERDE 406
                                                                                                                                                                                                                                                                                                                                                                                                                           407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 TYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPPYSE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 - QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 AECTNWNS----SALAQKPYSGR-----RPDAIRLGLGNHNYCRNPDRDSKPWCYV 192
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                                             111 AECTNWNS----SALAQKPYSGR-----RPDAIRLGLGNHNYCRNPDRDSKPWCYV 157
                                                                                                                                                                                             229 NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPEESP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTCEK 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09969271

Patent No. US20020098179A1

GENERAL INFORMATION:

APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));

APPLICANT: Pfizer Limited (GB and EP (GB) only);

TITLE OF INVENTION: Pnarmaceutical Combinations;

FILE REFERENCE: PCS10951APME

CURRENT APPLICATION NUMBER: US/09/969,271

CURRENT APPLICATION NUMBER: GB 0025473.0

PRIOR APPLICATION NUMBER: GB 0025473.0

PRIOR FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 562
                                                                                                                                         158 ---FKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY
                                                                                                                                                                                                                           179 PDQFK-GKF-----CEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENY
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24.0%; Score 755.5; DB 9; Length 5
Best Local Similarity 34.6%; Pred. No. 5.9e-51;
Matches 180; Conservative 78; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 DGTYYVYGIVSWGLECEKR -- PGVYTQVTKPLNWIKATIK 555
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/ ORGANISM: Homo sapiens

US-09-969-271-7
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US-09-969-271-7
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US-1U-411-037-26

| Sequence 26, Application US/10411037 |
| Publication No. US20040043446A1 |
| GENERAL INFORMATION |
| APPLICANT: DeFree, Shawn |
| APPLICANT: DeFree, Shawn |
| APPLICANT: DeFree, Shawn |
| APPLICANT: DeFree, Shawn |
| APPLICANT: Bayer, Robert |
| APPLICANT: Bayer, Bower |
| APPLICANT: Bayer, Bower |
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| APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYRGTWSTAESG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AECTNWNS----SALAQKPYSGR-----RPDAIRLGLGNHNYCRNPDRDSKFWCYV 192
289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCG 348
                                                         298 -----TCGLRQYSQPQF-RIKGGLFADIASHPWQAAIFAK--HRRSPGERFLCG 343
                                                                                                                                                349 GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEEFHEQSFRVQKIFKYSHYNERDE 406
                                                                                                                                                                                              344 GILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKXIVHKEFD--DD 401
                                                                                                                                                                                                                                                                                             407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 DGTYYVYGIVSWGLECEKR - - PGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 34.64
Matches 180; Conservative
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ORGANISM: Homo sapiens
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24.0%; Score 755.5; DB 10; Length 527;
34.6%; Pred. No. 546-51; DB 10
alve "by Mismatches 177; Indels 95; Gaps 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 PDQFK-GKF-----CEIGSDDCYVGDGYSYRGXMNTVNQHACLYWNSHLLLQENY 228
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FILE REPERINCE: 117-450 / N.79507A SER
CURRENT APPLICATION NUMBER: US/10/432,842
CURRENT FILING DATE: 2003-09-27
PRIOR APPLICATION NUMBER: CT/GB01/05244
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
NUMBER: OF SEQ. ID NOS: 2
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Publication No. US20040071707A1
GENERAL INPORMATION:
APPLICANT: Veronica A. CARROLL
APPLICANT: Adrian L. HARRIS
APPLICANT:
ROY BICKNELL
APPLICANT:
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NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 527
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                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 203, Application US/10360101

Sequence 203, Application US/10360101

GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICANT: Moll, Gert N.
APPLICATION NUMBER: US/10/360,101

CURRENT APPLICATION NUMBER: US/10/360,8

PRIOR APPLICATION NUMBER: US/203-02-7

RIOR PILNG DATE: 2002-05-24

NUMBER: PROPER PARENT: MOS: 309

SOFTWARE: Patentin version 3.1

FROM NO. 239

SEQ ID NO. 239

SEQ ID NO. 230
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                                                                                                                                                                  51 CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCEIDTRATCYEDQGISYRGTWSTAESG 110
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                                                                                                                         77 CQPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP--CGRG------ 123
                                                                                                                                                                                                                                     124 -QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATGSRHKRRSKFTCAC 178
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Query Match
Best Local Similarity 34.6%; Pred. No. 5.4e-51;
Matches 180; Conservative 78; Mismatches 177; Indels 85; Gaps
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Best Local Similarity 34.6%; Pred. No. 5.4e-51;
Matches 180; Conservative 78; Mismatches 177; Indels 95; Gaps
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US-10-360-101-203
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Gaps

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Indels

Length 527;

-QCLITQSPPYYRCVCKHPYTGPSCSQVVPVCRPNPCQ----NGATCSRHKRRSKFTCAC 178

21 124

77 CQPNPCEHGGDC--LVHGSTFTCSCLAPFSGNKCQ-KVQNTCKDNP--CGRG-

cch 24.0%; Score 755.5; DB 10; al Similarity 34.6%; Pred. No. 5.4e-51; 180; Conservative 78; Mismatches 177; 1

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CURRENT FILING DATE: 2001-11-14
PRICR APPLICATION NUMBER: 60/268,573
PRICR PILING DATE: 2001-02-15
PRICR APPLICATION NUMBER: GB 00 27 782.
PRICR APPLICATION NUMBER: GB 00 27 782.
PRICR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 18
LENGTH: 527
                                                                                                                                                       TYPE: PRT
, ORGANISM: Homo sapiens (tPA)
US-09-987-457-18
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Publication No. US20030013150A1

GENERAL INFORMATION:
APPLICANT: Manostoi, Aranya
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REFERENCE: 0652.2180001
CURRENT APPLICATION NUMBER: US/09/987,457
                                                                                                                                                                                                                                                                                                                                                                     20;
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24.0%; Score 756.5; DB 9; Length 562;
Best Local Similarity 34.6%; Pred. No. 4.9e-51;
Matches 180; Conservative 78; Mismatches 177; Indels 85
                                                                                                                                                                                                                                                             , NAME/KEY: misc feature
, OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
US-09-974-298-145
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                  APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENEE EXPRESSED IN BREAST CAN
TITLE OF INVENTION: GENEE EXPRESSED IN BREAST CAN
FILE REPERENCE: PA.037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOCTIMARE: PERL PROGRAM
SEQ ID NO 145
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
     GENERAL INFORMATION:
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US-09-987-457-18
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518 DGTYYVYGIVSWGLECEKR--PGVYTQVTKFLNWIKATIK 555

463 QLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPG-----QDTCQGDSGGPLTCEK

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GALIHPCWVLTAAHCTD--IKTRHLKVVLGDQDLKKEBFHEQSFRVQKIFKYSHYNERDB 309 GILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFD--DD 407 IPHNDIALLKLKPVDGHCALESKYVKTVCLP--DGSFPSGSECHISGWGVTETGKG--SR

349

289 TEPSTKLPGFDSCGKTEIAERKIKRIYGGFKSTAGKHPWQASLOSSLPLTISMPQGHFCG

229 NMFMEDAETHGIGEHNFCRNPDADEKPWCFIKVTNDKVKWEYCDVSACSAQDVAYPRESP

PDQFK-GKF------CEIGSDDCYVGDGYSYRGMMNRTVNQHACLYWNSHLLLQENY --- FKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVY

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APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Triedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: Methods for Large Scale Production
CURRENT PRILION: MAD-Derived tpA or K2S Molecules
FILE REFERENCE: 0652_2190001
CURRENT PAPLICATION NUMBER: US/09/997,455
CURRENT FILING DATE: 2001-11.14
PRIOR APPLICATION NUMBER: 60/268,574
FRIOR PILING DATE: 2010-12.15
PRIOR PILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
                        Sequence 19, Application US/09987455 Publication No. US20030049729A1 GENERAL INFORMATION:
US-09-987-455-19
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61 HAENPDWYYTEDQADPCQPNPCEHGGDCLVHGSTFTCSCLAPFSGNKCQKVQNTCKDNPC 120
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Pred. No. 4e-239;
1; Mismatches 1; Indels 0
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Best Local Similarity 99.6%;
Matches 558; Conservative 1
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127 ITQSPPYY-------RCVCKHPYTGPSCSQVV--PVCRPNPCQNGATCSRHK 169
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US-09-974-298-145
Sequence 145, Application US/09974298
; Patent No. US20020156263A1
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CRGANISM: Homo sapiens
US-10-172-712-28
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541 TOVTKFLNWIKATIKSESGF 560
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                                                                                                                                                                                                                                                                        TYPE: PRT
, ORGANISM: Homo sapiens
US-10-172-712-32
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APPLICANT: LANG, WIEGAND
APPLICANT: WEINER, THOMAS
APPLICANT: WEINER, THOMAS
APPLICANT: WEINER, THOMAS
APPLICANT: BERKER, MARGET
APPLICANT: BERLICH, CLAUDIA
APPLICANT: MUTHAN'S OF THE FACTOR VII-ACTIVATING PROTEASE AND TILLE OF INVENTION: MUTHAN'S OF THE FACTOR VII-ACTIVATING PROTEASE AND TILLE OF INVENTION: MUTHAN'S OF THE FACTOR VII-ACTIVATING PROTEASE AND TILLE REFERENCE: 06478.1457
CURRENT APPLICATION NUMBER: US/09/912,559
CURRENT FILING DATE: 2001-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR PLICATION NUMBER: DE 100 50 440.4
PRIOR FILING DATE: 2000-10-10
PRIOR PLICATION NUMBER: DE 100 52 319.6
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-41
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VEY: 2.1
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99.7%; Score 3143; DB 9; Length 560;
Best Local Similarity 99.6%; Pred. No. 4e-239;
Matches 558; Conservative 1; Mismatches 1; Indels
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, ORGANISM: Homo sapiens
US-09-912-559-3
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RESULT 6 US-10-172-712-32

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Sequence 32, Application US/10172712

PUBLICANT: GENERAL INFORMATION:
APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: GALE, ANDREW J.
APPLICANT: BELEGUER, JEAN-LUC
TITLE OF INVENTION: STABILIZED PROTEINS WITH ENGINEERED DISULFIDE BOND
FILE REPERANCE: 4198-4001US1
CURRENT APPLICATION NUMBER: US/10/172,712
CURRENT APPLICATION NUMBER: 00/298,578
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 32
LENGTH: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.7%; Score 3143; DB 14; Length 560;
Best Local Similarity 99.6%; Pred. No. 4e-239;
Matches 558; Conservative 1; Mismatches 1; Indels 0;
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Sequence 5, Application US/10391215
Publication No. US20040009543A1
GENERAL INFORMATION:
APPLICANT: KIECHL, STEFAN
APPLICANT: WILLEIT, JOHANN
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CGKTEIABRKIKRIYGGFKSTAGKHPWQASLQSSLPLTISMPQGHFCGGALIHPCWVLTA
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CURRENT APPLICATION NUMBER: US/10/391,215
CURRENT FILING DATE: 2003-03-19
PRIOR APPLICATION NUMBER: 09/912,559
PRIOR FILING DATE: 2001-07-26
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR APPLICATION NUMBER: DE 100 52 319.6
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: DE 100 52 319.6
PRIOR FILING DATE: 2001-0-1
PRIOR FILING DATE: 2001-0-1
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
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GENERAL INFORMATION:
APPLICANT: ROEMISCH, JUERGEN
APPLICANT: STOCHER, HANS-ARNOLD
APPLICANT: FEUSSNER, ANNETTE
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US-09-912-559-3
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APPLICANT: WILLEIT, JOHANN
APPLICANT: WIEDENANN, CHRISTIAN JOSEF
APPLICANT: WIEDENANN, CHRISTIAN JOSEF
APPLICANT: WEIMER, HOWAS
APPLICANT: PEUSSNER, ANNETTE
APPLICANT: STOEHR, HANS-ARNOLD
APPLICANT: DOERSAM, VOLKER
TITLE OF INVENTION: MARBURG I MUTANT OF FACTOR VII ACTIVATING PROTEASE
FILE REPERENCE: 06478.1457-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFKGKFCEIGSDDCYVGDGYSYRGKMNRTVNQHACLYWNSHLLLQENYNMFMEDAETHGI
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           52 319.6
       PRIOR APPLICATION NUMBER: DE 100 52 319
PRIOR FILIND DATE: 2000-10-21
PRIOR APPLICATION NUMBER: DE 101 18 700
PRIOR FILING DATE: 2001-04-12
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
IENGTH: 560
TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 100.0%; Pred. No. 6.5e-240;
tes 560; Conservative 0; Mismatches 0;
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APPLICANT: KIECHL, JOHANN
APPLICANT: WILLEIT, JOHANN
APPLICANT: WILLEIT, JOHANN
APPLICANT: WIEDERWANN, CHRISTIAN JOSEF
APPLICANT: WEDERCHANN, CHRISTIAN JOSEF
APPLICANT: WEDENSTRE, ANGETTE
APPLICANT: FEUSSNER, ANGETTE
APPLICANT: FORENSAM, VOIKER
TITLE OF INVENTION: MARBIRG I MUTANT OF FACTOR VII
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ART;
TITLE OF INVENTION: (FSAP) AS RISK FACTOR FOR ART;
TITLE OF INVENTION WHERE: US/10/391,215
CURRENT FILING DATE: 2003-03-19
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR APPLICATION NUMBER: DE 100 36 641.4
PRIOR APPLICATION NUMBER: DE 100 50 040.4
PRIOR FILING DATE: 2000-07-26
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US-10-391-215-8
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| Sequence 8, Application US/10391215
| Publication No. US20040009543A1
| GENERAL INFORMATION |
| APPLICANT: KIECHL, STEFAN |
| APPLICANT: WILLEIT, JOHANN |
| APPLICANT: WILLEIT, JOHANN |
| APPLICANT: WILLEIT, JOHANN |
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| APPLICANT: WILLEIT, JOHANN |
| APPLICANT: WILLEIT, JOHANS ARNOLD |
| APPLICANT: WILLEIT, JOHANS ARNOLD |
| APPLICANT: DOERSAM, VOLKER |
| TITLE OF INVENTION: MARBER: US/10/391,215 |
| TITLE OF INVENTION: (FGAP) AS RISK FACTOR FOR ARTERIAL THROMBOSIS |
| TITLE OF INVENTION NUMBER: US/10/301,215 |
| CURRENT APPLICATION NUMBER: DE 100 50 401.4 |
| PRIOR FILING DATE: 2000-07-26 |
| PRIOR FILING DATE: 2000-10-10 |
| PRIOR FILING DATE: 2000-10-10 |
| PRIOR APPLICATION NUMBER: DE 100 52 319.6 |
| PRIOR PILING DATE: 2000-10-10 |
| PRIOR APPLICATION NUMBER: DE 101 18 706.8 |
| PRIOR PILING DATE: 2001-04-12 |
| NUMBER OF SEQ ID NOS: 8 |
| SEQ ID NOS: 8 |
| SEG ID NOS: 8 |
| SEMPLICANT ON NUMBER: DE 10 50 40.4 |
| SEQ ID NOS: 8 |
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                                     1 MFARMSDLHVLLLMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYBDYNQBENTSSTLT
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        MFARMSDLHVLLLIMALVGKTACGFSLMSLLESLDPDWTPDQYDYSYEDYNQEENTSSTLT
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1 MPARMSDLHVLLLMALVGKT......TQVTKFLNWIKATIKSESGF
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12 US-10-411-026-26
14 US-10-193-656-8
16 US-10-410-962-26
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15 US-10-411-049-26
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17 US-09-084-4913-2
18 US-10-172-712-30
18 US-09-084-4913-2
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ase : PUDLISHEd APPLICATIONS AA: * 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:* 2: /cgn2_6/ptodata/1/pubpaa/US07_BFW_PUB.pep:* 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:* 4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:* 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:* 6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:* 7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:* 9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:* 9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:* 9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:* 9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*	Application US/09912559 S20020142316A1 REMATION
11: /cgnzb/prodata/1/pubpa/ususy-brecoms. 12: /cgnz_6/ptodata/1/pubpa/ususy-brecoms.pep:* 13: /cgnz_6/ptodata/1/pubpaa/usus/PuBcOMB.pep:* 14: /cgnz_6/ptodata/1/pubpaa/usus/PuBcOMB.pep:* 15: /cgnz_6/ptodata/1/pubpaa/usus/PuBcOMB.pep:* 17: /cgnz_6/ptodata/1/pubpaa/usus/PuB.pep:* 17: /cgnz_6/ptodata/1/pubpaa/usus/PuB.pep:* 18: /cgnz_6/ptodata/1/pubpaa/use0_NEW_PUB.pep:*	APPLICANT: FINSTAND ANNETTE APPLICANT: FINSTAND ANNETTE APPLICANT: LANG, WIEGAND APPLICANT: HOMAS APPLICANT: BECKER, MARGRET APPLICANT: WEIMER, THOMAS APPLICANT: WITH NAUMANN, GUDRUM TITHE OF INVENTION: MITTAND OF THE FACTOR VII-ACTIVATING PROTEASE
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES; FILE REFERENCE: 06478.1457; CURRENT APPLICATION NUMBER: US/09/912,559; CURRENT PILING DATE: 200.07-26; CURRENT PILING DATE: 200.07-26
SUMMARIES \$ 1t Query O. Score Match Length DB ID Description	
1 3153 100.0 560 9 US-09-912-559-4 Sequence 4, Appli 2 3153 100.0 560 15 US-10-391-215-8 Sequence 8, Appli 3 3150 99.9 560 15 US-10-391-215-6 Sequence 6, Appli 5 3146 99.8 560 15 US-10-391-215-6 Sequence 7, Appli 5 3143 99.7 560 19 US-09-912-559-3 Sequence 7, Appli 7 3143 99.7 560 14 US-10-172-172-32 Sequence 32, Appli 8 21:5 26.1 655 14 US-10-391-215-5 Sequence 28, Appli 9 755, 5 24, 0 55, 9 US-09-994-299-145 Sequence 145, Appli 9 755, 5 24, 0 527 10 US-09-994-299-145 Sequence 145, Appli 9 755, 5 24, 0 527 10 US-09-994-299-145 Sequence 145, Appli 9 755, 5 24, 0 527 10 US-09-994-298-145 Sequence 145, Appli 9 755, 5 24, 0 527 10 US-09-994-298-145	PRIOR AFFLING DATE: 2000-10-21
755.5 24.0 527 10 US-09-987-455-19 755.5 24.0 527 12 US-10-4360-11 755.5 24.0 527 15 US-10-360-101-203 755.5 24.0 562 9 US-09-969-271-7 755.5 24.0 562 12 US-10-411-037-26	ppl Query Match 100.0%; Score 3153; DB 9; Length 560; pli Best Local Similarity 100.0%; Pred. No. 6.5e-240; Matches 560; Conservative 0; Mismatches 0; Indels 0; ppl

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Gaps

Result No.

Search completed: May 24, 2004, 09:58:58 Job time : 43 secs